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06 August 1999

Date

Tina R. Wilson

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Docket No. 64-99

PATENT APPLICATION TRANSMITTAL LETTER

To the Commissioner of Patents and Trademarks:

Transmitted herewith for filing under 35 U.S.C. 111 and 37 C.F.R §1.53 is the patent application of:
Anna Kate Ursula KARA, Robert Chin Yao TING, Jill Maelan THAM, James Stuart NELSON and Theresa May Chin TAN

entitled: **DIAGNOSIS OF PLASMODIUM INFECTION BY ANALYSIS OF EXTRACHROMOSOMAL GENETIC MATERIAL**

Jc594 U.S. PTO
09/369992
08/06/99

Enclosed are:

- ☒ 77 pages of written description, claims and abstract
- ☒ 36 sheets of drawings
- ☐ pages of Sequence Listing as paper copy
- ☐ an assignment of the invention to _____
- ☐ executed declaration of the inventors and power of attorney
- ☐ a certified copy of a _____ application
- ☐ associate power of attorney
- ☐ a verified statement to establish small entity status under 37 CFR §1.9 and §1.27
- ☐ information disclosure statement
- ☒ preliminary amendment
- ☐ Sequence Listing diskette, statement under 37 C.F.R. 1.821-1.824

CLAIMS AS FILED

	Number Filed	Number Extra	Rate	Fee
BASIC FEE			\$760	\$760
TOTAL CLAIMS	44-20=	24	x \$18	432
INDEPENDENT CLAIMS	9-3=	6	x \$78	468
MULTIPLE DEPENDENT CLAIM PRESENT			x \$260	

* Number extra must be zero or larger

TOTAL \$1,660

If applicant has small entity status under 37 C.F.R. 1.9 and 1.27, then divide total fee by 2, and enter amount here.

SMALL ENTITY TOTAL

\$830

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— A check in the amount of \$_____ to cover the filing fee is enclosed.
— The Commissioner is hereby authorized to charge and credit Deposit Account No. 07-1969 as described below. A duplicate copy of this sheet is enclosed.

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— Charge any processing fees required under 37 CFR 1.17.
— Charge the issue fee set in 37 CFR 1.18 at the mailing of the Notice of Allowance, pursuant to 37 CFR 1.311(b).
— Other _____

X Benefit of Prior PCT Application(s) (35 USC 111)

Applicant claims priority under 35 USC 111 to the following application(s):

PCT/IB98/00212 filed 05 February 1998

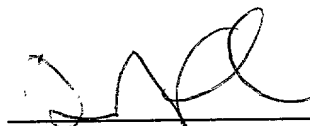
X Benefit of Prior PCT Application(s) (35 USC 119)

Applicant claims priority under 35 USC 119 to the following application(s):

Australian Patent Application PO4953/97, filed 06 February 1997

Australian Patent Application PO6329/97, filed 21 April 1997

Australian Patent Application PO9481/97, filed 26 September 1997



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Docket No.: 64-99
trw:August 6, 1999

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: :
Kara et al. : Group Art Unit: Unassigned
Serial No. Unassigned : Examiner: Unassigned
Filed: 06 August 1999 :
For: DIAGNOSIS OF PLASMODIUM :
INFECTION BY ANALYSIS OF
EXTRACHROMOSOMAL GENETIC
MATERIAL

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06 August 1999
Date

Tina R. Wilson
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PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

Please amend the above-identified patent application as follows:

In the Specification:

At page 1, between "DIAGNOSIS OF PLASMODIUM INFECTION BY ANALYSIS OF EXTRACHROMOSOMAL GENETIC MATERIAL" AND "FIELD OF THE INVENTION", please insert the following:

--

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims priority from International Application PCT/IB98/00212, filed February 5, 1998, which designates the United States and which claims priority from Australian Patent Application PO9481/97, filed September 26, 1997, Australian Patent Application PO6329/97, filed April 21, 1997 and Australian Patent Application PO4953/97, filed February 6, 1997. --

At page 9, line 28, please rewrite "Figure 9 is a copy of" and insert therefor --Figures 9A-9J present--.

At page 10, line 6, please delete "Figure 10 is" and insert therefor --Figure 10A-10N depict--.

At page 15, line 2, please delete "Figures 9 or 10" and replace with --Figures 9A-9J or 10A-10N--.

At page 15, line 7, please delete "Figures 9 or 10" and replace with --Figures 9A-9J or 10A-10N--.

At page 16, line 7, please rewrite "Figure 9" as --Figures 9A-9J--.

At page 22, line 25, please delete "Figures 9 or 10" and replace with --Figures 9A-9J or 10A-10N--.

At page 23, line 15, please delete "Figures 9 or 10," and replace with --Figures 9A-9J or 10A-10N,--.

At page 28, line 6, please delete "Figures 9 or 10" and replace with --Figures 9A-9J or

10A-10N--.

At page 26, line 26, please delete "Figure 9" and replace with --Figures 9A-9J--.

At page 26, line 26, please delete "Figure 10" and replace with --Figures 10A-10N--.

At page 45, line 23, please rewrite "(Figure 9)." as --(Figures 9A-9J).--.

In the Claims:

Please amend claims 1-44 (as presented under PCT Article 34 during International Phase of this application) as follows:

In claim 5, first line, please delete "any one of claims 1 to 4" and replace with --claim 1--.

In claim 6, first line, please delete "any one of claims 1 to 4" and replace with --claim 1--.

In claim 7, first line, please delete "any one of claims 1 to 4" and replace with --claim 1--.

In claim 8, first line, please delete "any one of claims 1 to 7" and replace with --claim 1--.

In claim 10, first line, please delete "any one of claims 1 to 7" and replace with --claim 1--.

In claim 12, first line, please delete "or 11".

In claim 13, first line, please delete "any one of claims 1 to 12" and replace with --claim 1--.

In claim 14, first line, please delete "any one of claims 1 to 13" and replace with

--claim 1--.

In claim 21, first line please delete “any one of claims 16 to 20” and replace with --claim 16--.

In claim 22, first line, please delete “any one of claims 16 to 20” and replace with --claim 16--.

In claim 23, first line, please delete “any one of claims 16 to 20” and replace with --claim 16--.

In claim 24, first line, please delete “any one of claims 16 to 20” and replace with --claim 16--.

In claim 26, first line, please delete “any one of claims 16 to 23” and replace with --claim 16--.

In claim 28, first line, please delete “claims 26 or 27” and replace with --claim 26--.

In claim 40, second and third lines, please delete “any one of claims 33 to 38” and replace with --claim 33--.

In claim 40, third line, please delete “the primer pairs according to claims 39 or 40” and replace with --a primer pair comprising at least one of said primers--.

In claim 42, second and third lines, please delete “any one of claims 34 to 37” and replace with --claim 34--.

In claim 42, third line, please delete “the primer pairs according to claims 38 or 39” and

replace with --a primer pair comprising at least one of said primers--.

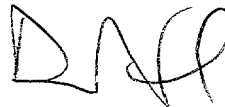
In claim 43, first line, please delete "any one of claims 40 to 42" and replace with --claim 40--.

Please enter new claim 45:

-- 45. The kit according to claim 42 comprising one or more isolated primer pairs, wherein both primers of a primer pair is provided in the same compartment at a relative concentration suitable for the amplification of plastid DNA or plastid-like DNA or mitochondrial *coxI* sequences form a *Plasmodium* malarial agent of humans contained in a blood sample or derivative thereof. --

It is believed that the present submission does not require the payment of any fee under 37 C.F.R. 1.16-1.17. If this is incorrect, please charge any necessary fee and any extensions of time required to Deposit Account No. 07-1969.

Respectfully submitted,



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Attorney Docket No. : 64-99
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FIELD OF THE INVENTION

The present invention relates generally to novel genetic sequences isolated from a parasitic
5 protozoa which infects humans and other animals and the uses of said sequences as diagnostic
agents for the detection of said protozoa in a biological sample. In particular, the present
invention provides genetic sequences of the extrachromosomal genetic elements of the malaria
agents *Plasmodium berghei*, *Plasmodium vivax*, *Plasmodium ovale*, *Plasmodium falciparum*
and *Plasmodium malariae* and synthetic oligonucleotide derivatives, homologues, analogues
10 and fragments thereof. The genetic sequences of the present invention are particularly useful
in the diagnosis, prophylactic treatment and therapeutic treatment of humans and other
animals which are capable of being infected by or are actually infected by protozoa such as
Plasmodium ssp., for example *P. falciparum*, *P. vivax*, *P. malariae*, *P. ovale*, *P. cynomolgi*,
P. gonderi, *P. (Hepatocytis) kochi*, *P. inui*, *P. knowlesi*, *P. reichenowi*, *P. rodhaini*, *P.*
15 *schwetzi*, *P. cathemerium*, *P. elongatum*, *P. relictum*, *P. lophurae*, *P. gallinaceum*,
P. chabaudi, *P. yoelii*, or *P. berghei*, amongst others. The invention provides further, a
novel, reliable diagnostic assay for the detection of *Plasmodium ssp.* in humans and animals.

Bibliographic details of the publications referred to by author in this specification are
20 collected at the end of the description. Sequence identity numbers (SEQ ID Nos.) for the
nucleotide and amino acid sequences referred to in the specification are defined after the
bibliography.

Throughout the specification, unless the context requires otherwise, the word "comprise", or
25 variations such as "comprises" or "comprising", will be understood to imply the inclusion of
a stated element or integer or group of elements or integers, but not the exclusion of any
other element or integer or group of elements or integers.

BACKGROUND TO THE INVENTION

30 More than fifty different species of *Plasmodium* can cause malaria in humans, monkeys,

birds, fish, cattle and rodents. The development of diagnostic assays for the detection of *Plasmodium* in humans and animals is therefore highly desirable.

Human malaria, which is caused by *Plasmodium ssp.*, in particular *P. falciparum*, *P. vivax*,
5 *P. malariae*, and *P. ovale*, remains one of the major health problems around the world.

Plasmodium vivax induces a moderate form of malaria, vivax malaria, characterized by periodic chills and fever, an enlarged spleen, anaemia, severe abdominal pain and headaches, and extreme lethargy. If left untreated, the disease tends to be self-limiting within a period
10 of 10 to 30 days, but will recur periodically. Although the fatality rate of vivax malaria is low, the disease is highly debilitating and makes the patient more vulnerable to other diseases.

The incubation period ranges from 10 days to 4 weeks. Generally, paroxysms of chills and fever appear on the 14th day after the bite of an infected female anopheles mosquito. During
15 this time the parasite has been multiplying in the liver cells of the patient. Paroxysms continue to recur every other day, as the parasite completes its 48-hour cycle of development, now in the blood. During the paroxysm, the patient first goes through a "cold stage" during which he has chilly sensations, his skin is blue, his teeth chatter and there is violent shaking. After an hour, the "hot stage" is ushered in, with a rise in temperature to as high as 107°F
20 (41.7°C); the skin is hot and dry and the patient complains of severe headache. The fever lasts about 2 hours, and is followed by the "sweating stage", during which there is profuse perspiration, the temperature falls to normal, the headache disappears, and although weak and drowsy, the patient feels well.

25 *Plasmodium ovale* produces a disease very similar to vivax malaria.

Plasmodium malariae, the causative agent of quartan malaria, has an incubation period of 18-40 days. The paroxysms occur every 72 hours, and are longer and somewhat more severe than those accompanying vivax malaria.

Plasmodium falciparum-induced malaria (falciparum malaria) presents oedema of the brain and lungs and blockage of the kidneys, in addition to the symptoms associated with vivax malaria. Unless treated promptly, the fatality rate of falciparum malaria is high, especially in juveniles.

5

Paroxysms associated with falciparum malaria occur irregularly after a 12-day incubation period. They are severe, and accompanied by high temperatures. The so-called cerebral algid, haemorrhagic and pernicious types of malaria represent forms of falciparum malaria with different localizations of the parasite. In the cerebral type, the onset is delirium and
10 coma, and death may occur in several hours without return to consciousness. "Black-water fever" or haemorrhagic malaria is a type in which haemolysis or dissolution of the red cells occurs, and dark urine due to the presence of haemoglobin is an outstanding feature. In the algid form, there are vomiting, diarrhea, and subnormal temperature.

15 The life cycle of the parasite and its course in the human body proceeds in the following way. The saliva of the mosquito contains the *Plasmodium* at the lance-shaped sporozoite stage of its life cycle. Upon inoculation of the host by biting, the sporozoites quickly migrate to the liver where they divide and develop into multi nucleated schizonts. Within 6 to 12 days, the schizonts disrupt and release into the blood the form known as *merozoites*. Each liver cell
20 infected by one sporozoite releases into the blood stream from 10,000 to 30,000 merozoites. These later invade the host's erythrocytes where they grow and form more schizonts which, in turn, again divide, releasing more merozoites into the blood stream to repeat the cycle. The principal symptoms of malaria are associated with the rupture of the schizonts, the periodic lysis of the blood cells with release of merozoites and toxic wastes which cause the
25 regular fevers and chills of malaria.

Neither vector control measures nor immuno or chemoprophylaxis have proven effective in eradicating the disease. Thus, more than ever, chemotherapy appears to be crucial in dealing with both the prevention and treatment of malaria. However, presently used drugs are
30 constantly losing their efficacy due to the development of drug resistance by the parasite. For

example, drug resistance of *Plasmodium falciparum* to chloroquine has occurred in Bangladesh, Brazil, Burma, Colombia, Ecuador, Guyana (French), Guyana, India, Indonesia, Kampuchea, Malaysia, Nepal, Pakistan, Panama, Philippines, Surinam, Thailand, Venezuela, and Vietnam, amongst others. Therefore, the design of novel drugs is urgent.

5

Targets for drug design are generally nuclear-encoded gene products. However, inter-specific and developmental variation in nuclear gene expression has reduced the general efficacy of drugs which target such nuclear-encoded gene products.

- 10 Diagnosis of malaria is generally made by microscopic examination of blood films taken during episodes of fever, when the parasites may be seen. In general, the *Plasmodium* parasite is detected microscopically by examining finger prick blood samples for the presence of the morphologically distinct parasite using Giemsa stain solution (Shute *et al.*, 1980). This needs to be done by an experienced microscopist since *Plasmodium falciparum* and
- 15 *Plasmodium vivax* are morphologically similar, albeit not identical. In view of the distinct epidemiologies of *P. falciparum* compared to *P. vivax*, it is important that diagnosis of infection by these species have a low error rate. Any incorrect diagnosis of falciparum malaria, for example, may be fatal for the patient. The microscopic technique is limited in so far as the method is slow and specialised personnel is required to perform the technique.

20

A variation of the standard microscopic assay, the quantitative buffy coat (QBC) technique is based upon the ability of parasite nucleoproteins to absorb acridine orange and fluoresce (Wardlaw *et al.*, 1983). The fluorescent nucleoproteins are readily visible against a background of non-fluorescent red blood cells. Although the method is more sensitive than

25 the standard microscopic assay, it suffers from the disadvantages associated with the standard microscopic assay. Furthermore, the requirement of costly fluorescence microscopes and centrifuges to perform the QBC assay, renders the method unrealistic in resource-limited settings which often lack even electricity.

- 30 Immunological tests, for example the ParaSight™ F test (Becton Dickinson) and the similar

ICT Malaria P.f. test (ICT Diagnostics) detect the *Plasmodium falciparum* histidine-rich protein HRP2 in blood samples derived from patients. A major drawback associated with such methods is that they require *Plasmodium falciparum* gene expression to occur before the organism can be detected. Furthermore, as considerable variation in gene expression can occur between *Plasmodium ssp.*, these tests tend to be species-specific. For example, the ParaSight™ F test (Becton Dickinson) and ICT Malaria P.f. test (ICT Diagnostics) are specific for *Plasmodium falciparum* only and incapable of detecting other species. Furthermore, these tests, in particular the ParaSight™ F test (Becton Dickinson), are subject to a high proportion of false-negative detections, such that a higher than acceptable frequency of patients infected with a *Plasmodium ssp.* go undetected.

Immunological techniques such as the enzyme-linked immunosorbent assay (ELISA) or the radio immunoassay (RIA) which detect genus- and species-specific parasite antigens also exist. However, such methods are constrained by immunological cross-reaction between parasite and host antigens on the one hand and between parasite antigens and antigens derived from other microorganisms on the other hand. As a consequence, the susceptibility of immunological methods to false positive detection of *Plasmodium* is high. As already mentioned above, species-specific detection methods lead to a large number of false-negative detections.

20

Furthermore, as different *Plasmodium* antigens are expressed at different developmental stages, immunological techniques may only detect the parasite at certain stages of development. Such antigenic diversity displayed by *Plasmodium* is a major obstacle to the application of immunological techniques. In addition, radioisotope-based assays such as the RIA are impractical for field use. Immunological methods cannot distinguish between past and present infections.

State-of-the art diagnostic assays, which rely on the detection of *Plasmodium* genomic DNA in a sample, are species-specific and not capable of general application for any *Plasmodium ssp.*, in part because there is considerable variation in genomic DNA between *Plasmodium*

30

species, such variation precluding the simultaneous detection of several *Plasmodium ssp.* in a single biological sample or alternatively, the use of a single DNA-based assay for the detection of any *Plasmodium ssp.* in a biological sample derived from a human or animal subject suspected of carrying the parasite.

5

As a consequence of the foregoing, there is a high demand for a reliable and simple technology for the diagnosis of *Plasmodium* in human and animal tissues.

Plasmodium ssp. possess additional genomes with potentially crucial functions (Wilson *et al.*, 10 1991). Until the present invention, very little was known about this extrachromosomal material. Furthermore, the function of the extrachromosomal plastid element in the protozoans remains to be determined. To date, there is no clear evidence for DNA replication or functionally active gene products from the plastid element.

15 SUMMARY OF THE INVENTION

One aspect of the present invention provides a method of detecting a *Plasmodium* in a biological sample derived from a human or animal subject, said method comprising contacting a *Plasmodium* extrachromosomal genetic element or a fragment thereof with said sample or nucleic acid derived therefrom for a time and under conditions sufficient for hybridisation to 20 occur and then detecting said hybridisation using a detection means. According to this aspect, the extrachromosomal genetic element or fragment thereof may comprises a mitochondrion or mitochondrion-like molecule or a genetic sequence derived therefrom or a homologue, analogue or derivative thereof, in particular a *Plasmodium* cytochrome C oxidase (coxI) genetic sequence derived from any one of *P. falciparum*, *P. berghei*, *P. vivax*, *P. ovale* or *P. malariae*, 25 amongst others.

Alternatively, the extrachromosomal genetic element may comprise a plastid or plastid-like molecule or a genetic sequence derived therefrom or a homologue, analogue or derivative thereof, in particular a *Plasmodium* PS1-PL470, PLH-PPH, PRB or PWQ genetic sequence 30 derived from *P. falciparum*, *P. berghei*, *P. vivax*, *P. ovale* or *P. malariae*, amongst others.

Preferably, the detection means comprises a nucleic acid hybridisation reaction or polymerase chain reaction or a modification thereof, essentially as described herein.

A further aspect of the invention provides for the use of said *Plasmodium* extrachromosomal genetic element or a homologue, analogue or derivative thereof to detect *Plasmodium* in a biological sample derived from a human or animal, for example a biological sample comprising blood or blood products, in particular dried blood.

A further aspect of the invention provides an isolated extrachromosomal genetic element primer or probe derived from *Plasmodium* *ssp.*

A further aspect of the invention provides a kit for the detection of *Plasmodium* *ssp.* in a biological sample, said kit comprising one or more isolated extrachromosomal genetic element probes or primers and one or more reaction buffers suitable for use in a nucleic acid hybridisation reaction or polymerase chain reaction.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a copy of a photographic representation of an electron micrograph of the *Plasmodium berghei* extrachromosomal plastid preparation. P denotes the *P.berghei* plastid while M is pBR322 (4.36 kb) used as a size marker. The bar represent the size of 1 kb.

Figure 2 is a copy of a photographic representation showing the *EcoRI* and *HindIII* restriction digests of *Plasmodium berghei* extrachromosomal plastid DNA. In panel (a), plastid DNA was digested with 20 units of *EcoRI* (New England Biolabs (NEB), Beverly, MA, USA) in a reaction mixture of 10 uL. The digested products were separated on a 0.4% (w/v) agarose gel at 120 V for 6 hours. Lane 1 shows Lambda Monocut markers (NEB, USA); lane 2 the *EcoRI* digest resulting in three fragments (E1, E2 and E3); lane 3 shows Lambda DNA-*Hind* III digest markers (NEB, USA); and lane 4 shows Lambda DNA-*BstEII* digest markers (NEB, USA). Panel (b) shows a *HindIII* digest of the extrachromosomal element of *P.berghei*. The digested products were separated on a 0.6 % (w/v) agarose gel at 100 V for

6 hours. Lane 1 shows Lambda DNA-*Bst*EII digest markers (NEB, USA); lane 2 shows a *Hind*III digest of *P. berghei* DNA resulting in six fragments (H1, H2, H3, H4, H5 and H6); and lane 3 shows Lambda DNA-*Bst*EII digest markers (NEB, USA).

5 **Figure 3** is a copy of a photographic representation of a Southern Hybridization of *Hind*III and *Hind*III /*Eco*RI digests of the *Plasmodium berghei* extrachromosomal element. Panel (a) shows restriction digests of *P. berghei* extrachromosomal DNA. Lane M1 shows the 123 bp DNA marker (Gibco-BRL); lane HE the *Hind*III /*Eco*RI digest resulting in 8 fragments (H2, H3, H4, HE1, H5, HE2, E1 and E2); lane H the *Hind*III digest resulting in 6 fragments, H2, 10 H3, H4, H5 and H6); lane M2 the Lambda DNA-*Hind*III digest markers (NEB, USA); and lane M3 the Lambda DNA-*Bst*EII digest markers (NEB, USA). Panel (b) shows a Southern hybridization of the fragments in panel (a) with probe PS 1. Panel (c) shows a Southern hybridization of the fragments in panel (a) with probe PL470. Panel (d) shows a Southern hybridization of the fragments in panel (a) with probe PWQ.

15

Figure 4 is a representation of the physical and genetic map of the *Plasmodium berghei* circle. Panel (a) is a schematic representation of the arrangement of various genes and the *Eco*RI and *Hind*III sites are shown. The three *Eco*RI fragments, E1, E2 and E3 as well as the *Hind*III fragments H1, H2a, H2b as well as H4 are shown. Fragment H6 comprises of HE1, 20 E1, E2 and HE2. The relative position of the various PCR products (Table 1) is also indicated as solid bars. Panel (b) shows a comparison between homologous genes on the *Plasmodium falciparum* and *Plasmodium berghei* plastid circles and tRNA genes are specified by a single letter amino-acid code.

25 **Figure 5** is a copy of a photographic representation showing RT-PCR analysis of *rRNAs* transcripts. Lane 1 and 6 show the 100bp DNA ladder (Promega), lanes 2 and 3 show the RT-PCR product (L) using a set of *lsu-rRNA* gene specific primers and lanes 4 and 5 show the product (S) using a set of *ssu-rRNA* gene specific primers respectively. The (-) lanes show reactions without the reverse transcriptase enzyme.

30

Figure 6 is a copy of a photographic representation showing PCR amplification products generated using the primer set L1/L2 (SEQ ID NO: 5/SEQ ID NO: 6) (Panel a), and the primer set DHFR1/DHFR2 (Panel b). Blood was drawn daily for 5 days from a mouse initially infected with 5×10^4 parasites. Lanes 1-5 in both panels show the amplification products obtained from blood spots 1 to 5 days post-infection correspondingly. Lane 6 is the negative control with blood from an uninfected mouse and lane 7 is the positive control using 50ng of purified *P.berghei* total DNA as template. M indicates the 100bp DNA ladder (Promega) used as markers.

Figure 7 is a copy of a photographic representation showing PCR amplification of blood spots from Laotian patients diagnosed positive for *P.falciparum* malaria by Giemsa microscopy and ParaF dipstick, with the exception of one which was infected with *P. vivax* (lane 11). Primers used were the L1/L2 primer set (i.e. SEQ ID NO: 5/SEQ ID NO: 6). Lane 12 is the negative control with a blood spot from a healthy person and lane 13 is the positive control using 50ng of purified *P.falciparum* (FC27 strain) total DNA as template. M indicates the 100bp DNA ladder (Promega) used as markers. The arrow indicates the position of amplified LSU DNA.

Figure 8 is a copy of a photographic representation showing PCR amplification of blood spots from uninfected persons using the L1/L2 (SEQ ID NO: 5/SEQ ID NO: 6) primer set (Top Panel) and AC1/AC2 primer set (Lower Panel). Lanes 1 and 2 in both top and lower panels are positive controls for human β -actin using 50ng of purified total DNA from CaSki and HeLa cells. Lanes 3-10 in both top and lower panels use blood spots from uninfected persons as the template. Lanes 11 and 12 in the lower panel use blood spots from a *P.falciparum*-infected patient and a *P.vivax*-infected patient respectively. M indicates the 100bp DNA ladder (Promega) used as markers.

Figure 9 is a copy of a schematic representation of the aligned LSU-rRNA sequences from different *Plasmodium* species obtained from various regions in Asia. The alignment was carried out using the Clustal Method in the DNASTAR programme. Sequences indicated are

derived from several isolates of *P.falciparum* (Pf), *P.vivax* (Pv), *P.malariae* (Pm), *P. Ovale* (Po) and *P.berghei* (Pb). The alphanumeric designation following the *Plasmodium* species descriptor indicates the isolate number and geographical origin of the specimen, wherein P=Pakistan, I=India, L=Laos, C=Columbia and S=Singapore. The GenBank accession
5 numbers for Pf(C10) and Pb(ANKA) are X95275 and U79731 respectively.

Figure 10 is a schematic representation of the aligned cox I sequences from *P.falciparum* (Pf), *P.vivax* (Pv), *P.malariae* (Pm) and *P. Ovale* (Po) isolates. The numeric designation following the *Plasmodium* species descriptor indicates the isolate number. The GenBank
10 accession number for the *P.falciparum* sequences is M76611.

Figure 11 is a copy of a photographic representation showing PCR amplification of blood spots. Each reaction uses 1 µl of blood containing different quantity of parasites. The amount of DNA used in each reaction, expressed as an equivalent number of parasites, is as follows: lane 1
15 contains 800 parasites; lane 2 contains 400 parasites; lane 3 contains 80 parasites; lane 4 contains 40 parasites; lane 5 contains 8 parasites; lane 6 contains 4 parasites; and lane 7 contains 0.8 parasites. Lane 8 contains the 100bp DNA ladder (Promega) used as a marker. The detection limit is 4 parasites.

20 DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

In work leading up to the present invention, the inventors have discovered that the molecular composition, physical arrangements and nucleotide sequences of the extrachromosomal plastid-like element and mitochondrial element are highly conserved in different *Plasmodium*
ssp.

25

The inventors have utilised the high degree of homology between different *Plasmodium* ssp. in the design of reliable, genera-specific or species-specific diagnostic assays for the detection of *Plasmodium*. The diagnostic assays described herein provide a significant advantage over

currently employed assays based upon the detection of *Plasmodium* genomic DNA.

Furthermore, the inventors have discovered that the assays described herein provide the added advantage of excluding the high frequency of false negative detection of *Plasmodium* in a
5 biological sample to a greater degree than known diagnostics.

The inventors further contemplate the use of polypeptides encoded by the extrachromosomal plastid-like element, and their homologues, analogues and derivatives, as targets for drug design and in the development of anti-malarial vaccines.

10

Accordingly, one aspect of the invention provides a diagnostic assay for the detection of *Plasmodium* in a biological sample derived from a human or animal subject, said assay comprising the detection of a *Plasmodium* extrachromosomal genetic element or a homologue, analogue or derivative thereof in said sample.

15

In an alternative embodiment, the invention provides a diagnostic assay for the detection of *Plasmodium* in a biological sample derived from a human or animal subject, said assay comprising the steps of hybridising a *Plasmodium* *ssp.* extrachromosomal genetic element probe or primer or a homologue, analogue or derivative thereof to said sample and then
20 detecting said hybridisation using a detection means.

According to this aspect, the *Plasmodium* detected using the invention may be any species of *Plasmodium* which carries an extrachromosomal genetic element.

25 In a preferred embodiment, the *Plasmodium* being detected is selected from the list comprising *P. falciparum*, *P. vivax*, *P. malariae*, *P. ovale*, *P. cynomolgi*, *P. gonderi*, *P. (Hepatocytis) kochi*, *P. inui*, *P. knowlesi*, *P. reichenowi*, *P. rodhaini*, *P. schwetzi*, *P. cathemerium*, *P. elongatum*, *P. relictum*, *P. lophurae*, *P. gallinaceum*, *P. yoelii*, or *P. berghei*, amongst others.

30

In a more particularly preferred embodiment however, the present invention is useful for the detection of a *Plasmodium* in biological samples derived from humans and the *Plasmodium* in such cases is selected from the list comprising *P. falciparum*, *P. vivax*, *P. malariae* and *P. ovale*, amongst others.

5

The term "biological sample" as used herein shall be taken to refer to any organ, tissue, cell, exudate, nucleic acid, protein, nucleoprotein or other material which is derived from a living or once-living organism. Accordingly, biological samples may be mosquito or other vectors of *Plasmodium* ssp., human or animal tissue, blood or derivatives of blood and blood
10 products, amongst others. A biological sample may be prepared in a suitable solution, for example an extraction buffer or suspension buffer. The present invention extends to the diagnosis of biological solutions thus prepared, the only requirement being that said solution at least comprises a biological sample as described herein.

15 The biological sample to be tested according to the invention, is derived from a human or animal species, in particular a human or animal which is capable of being infected by a *Plasmodium*. A particular advantage of the present invention is that it may be readily adapted to facilitate the analysis of any biological sample derived from a human or other animal. Those skilled in the relevant art will know how to modify the assay of the invention for the
20 purposes of adapting said assay to the analysis of different biological tissues, where relevant or indicated, without any undue experimentation.

In a particularly preferred embodiment, the biological sample may be derived from the blood tissue of a human or animal subject, or cells, nucleic acid molecules and exudates derived
25 therefrom, for example buffy coat, plasma, DNA or RNA, amongst others. The use of dried blood spots derived from human subjects as biological samples for the performance of the assays described herein is particularly contemplated by the invention.

The term "extrachromosomal genetic element" shall be taken to refer to any nucleic acid
30 molecule, in particular DNA or RNA, which comprises a part of the complete genetic

material of a *Plasmodium ssp.* but which does not comprise a part of a *Plasmodium ssp.* chromosome or a direct gene product thereof. An extrachromosomal genetic element of a *Plasmodium ssp.* may or may not replicate independently of the *Plasmodium* genome, such that the copy number of said genetic element may vary between *Plasmodium* cells.

5

Accordingly, a *Plasmodium* extrachromosomal genetic element as hereinbefore defined may be a linear or circular DNA molecule. In this regard, a linear DNA molecule may resemble, at the nucleotide sequence level at least, mitochondrial DNA (Suplick *et al*, 1988), while the circular DNA molecule in a *Plasmodium* resembles a vestigial plastid genome (Gardner *et al*,
10 1991; Howe *et al*, 1992).

The present inventors have shown herein that the malaria parasites harbour two extrachromosomal DNAs. One of these is a small 6 kb molecule which encodes three classical mitochondrial protein coding genes, attesting to its identity. The other is a circular
15 molecule resembling the remnant of an algal plastid genome. The mitochondria DNA of *Plasmodium* species is very short; about 6 kb and codes for three proteins, namely cytochrome *c* oxidase subunits I (cox I) and III (cox III), and cytochrome *b* (cyt *b*) as well as fragments of ribosomal RNA genes.

20 In a preferred embodiment of the invention, the *Plasmodium* extrachromosomal genetic element is a plastid DNA molecule comprising approximately 30-35kb of nucleotides in length.

In an alternative preferred embodiment, the *Plasmodium* extrachromosomal genetic element
25 is mitochondrial DNA or mitochondrion-like DNA comprising approximately 6 kb in length.

In the present context, an extrachromosomal genetic element may comprise a complete organellar DNA molecule or a derivative thereof, for example a gene or an oligonucleotide which is suitable for use as a probe or primer molecule.

30

As used herein, the term "probe" refers to a nucleic acid molecule which is derived from a *Plasmodium* extrachromosomal genetic element and capable of being used in the detection thereof.

- 5 The term "primer" refers to a probe as hereinbefore defined which is further capable of being used to amplify a nucleotide sequence derived from a *Plasmodium* extrachromosomal genetic element in a polymerase chain reaction.

The diagnostic assay of the present invention is useful for the detection of a *Plasmodium*
10 extrachromosomal genetic element or a *Plasmodium*-derived extrachromosomal genetic element, regardless of whether or not said genetic element expresses or is capable of expressing a polypeptide product.

The term "*Plasmodium*-derived" as used herein shall be taken to refer to an integer which,
15 although it originates from a *Plasmodium ssp.* is not necessarily present in its natural state. For example, an extrachromosomal genetic element may be derived from a *Plasmodium ssp.* if it has been purified or partially purified and/or modified by digestion with restriction endonucleases or other DNA-modifying enzymes, to produce an analogue or derivative molecule.

20

The *Plasmodium* extrachromosomal genetic element probe or primer may be a mitochondrion or mitochondrion-like molecule or alternatively a plastid or plastid-like molecule, derived from a *Plasmodium ssp.* which is capable of infecting a human or animal subject.

- 25 In a particularly preferred embodiment, the extrachromosomal genetic element probe or primer or a homologue, analogue or derivative thereof, is derived from *Plasmodium berghei*, *P. ovale*, *P. malariae*, *P. falciparum*, *Plasmodium vivax*, *Plasmodium malariae*, *Plasmodium chabaudi*, *Plasmodium yoelii*, amongst others.

- 30 However, in a more particularly preferred embodiment of the invention, the

extrachromosomal genetic element probe or primer is at least 95% identical to one or more of the sequences set forth in SEQ ID Nos: 1-22 or Figures 9 or 10 or a complementary nucleotide sequence, or a homologue, analogue or derivative thereof.

- 5 Alternatively, the extrachromosomal genetic element probe or primer is capable of hybridising under high stringency conditions to one or more of the sequences set forth in SEQ ID NOS: 1-22 or to any one or more of the sequences set forth in Figures 9 or 10 or a complementary nucleotide sequence or a homologue, analogue or derivative thereof.
- 10 In a further alternative embodiment, the *Plasmodium* spp. extrachromosomal genetic element probe or primer used in the inventive method preferably comprises a sequence of nucleotides of at least 15 nucleotides, more preferably at least 25 nucleotides, even more preferably at least 50 nucleotides and even more preferably at least 100 nucleotides or 500 nucleotides derived from the sequence set forth in SEQ ID NOS:1-4 or to the *Plasmodium vivax*,
15 *Plasmodium ovale*, *Plasmodium berghei*, *Plasmodium falciparum* or *Plasmodium malariae* sequences set forth in Figures 9 or 10, or a complement thereof.

In a most particularly preferred embodiment, the extrachromosomal genetic element probe or primer comprises a nucleotide sequence set forth in any one or more of SEQ ID NOS: 1-22
20 or Figures 9 or 10, or a complementary nucleotide sequence, or a homologue, analogue or derivative thereof.

For the purposes of nomenclature, the nucleotide sequences set forth in SEQ ID NOS:1-4 correspond to one strand of the PS1-PL470, PLH-PPH, PRB and PWQ genes, respectively,
25 of the 30.7 kb *Plasmodium berghei* plastid. The inventors have shown that the extrachromosomal genetic element is transcriptionally-active, using reverse transcription polymerase chain reaction (RT-PCR), and encodes organelle-like rRNAs, tRNAs, ribosomal proteins and RNA polymerase subunits, amongst others.

30 The nucleotide sequences set forth in SEQ ID Nos: 5-10 and 19-20 correspond to synthetic

oligonucleotide sequences derived from the *Plasmodium berghei* plastid.

The nucleotide sequences set forth in SEQ ID Nos: 11-14 and 22 correspond to synthetic oligonucleotide sequences derived from the *Plasmodium vivax* mitochondrial coxI gene, while
5 the nucleotide sequences set forth in SEQ ID Nos: 11, 15-18 and 21 correspond to synthetic oligonucleotide sequences derived from the *P. falciparum* mitochondrial coxI gene.

The nucleotide sequences Pm1/S and Pm38/S in Figure 9 relate to the plastid-like extrachromosomal genetic element in two *P. malariae* isolates and Po35/S and Po36/S relate
10 to the extrachromosomal genetic element of two *P. ovale* isolates. The nucleotide sequences designated Pv12/P, Pv13/P, Pv15/I, Pv16/L, Pv17/S and Pv86/C in Figure 9 relate to plastid-like extrachromosomal genetic element sequences of different *P. vivax* isolates.

For the present purpose, "homologues" of a nucleotide sequence shall be taken to refer to an
15 isolated nucleic acid molecule which is substantially the same as the nucleic acid molecule of the present invention or its complementary nucleotide sequence, notwithstanding the occurrence within said sequence, of one or more nucleotide substitutions, insertions, deletions, or rearrangements.

20 "Analogues" of a nucleotide sequence set forth herein shall be taken to refer to an isolated nucleic acid molecule which is substantially the same as a nucleic acid molecule of the present invention or its complementary nucleotide sequence, notwithstanding the occurrence of any non-nucleotide constituents not normally present in said isolated nucleic acid molecule, for example carbohydrates, radiochemicals including radio nucleotides, reporter molecules such
25 as, but not limited to biotin, DIG, alkaline phosphatase or horseradish peroxidase, amongst others.

"Derivatives" of a nucleotide sequence set forth herein shall be taken to refer to any isolated nucleic acid molecule which contains significant sequence similarity to said sequence or a part
30 thereof. Generally, the nucleotide sequence of the present invention may be subjected to

mutagenesis to produce single or multiple nucleotide substitutions, deletions and/or insertions. Nucleotide insertional derivatives of the nucleotide sequence of the present invention include 5' and 3' terminal fusions as well as intra-sequence insertions of single or multiple nucleotides or nucleotide analogues. Insertional nucleotide sequence variants are those in
5 which one or more nucleotides or nucleotide analogues are introduced into a predetermined site in the nucleotide sequence of said sequence, although random insertion is also possible with suitable screening of the resulting product being performed. Deletional variants are characterised by the removal of one or more nucleotides from the nucleotide sequence. Substitutional nucleotide variants are those in which at least one nucleotide in the sequence
10 has been removed and a different nucleotide or nucleotide analogue inserted in its place.

The present invention encompasses all such homologues, analogues or derivatives of a *Plasmodium* extrachromosomal genetic element, subject to the proviso that said homologues, analogues or derivatives are useful in the performance of at least one assay format as
15 described herein.

According to this aspect of the invention, the *Plasmodium* extrachromosomal genetic element probe or primer may comprise inosine, adenine, guanine, thymidine, cytidine or uracil residues or functional analogues or derivatives thereof which are capable of being
20 incorporated into a polynucleotide molecule, provided that the resulting probe or primer is capable of hybridising under at least low stringency conditions to a *Plasmodium* extrachromosomal genetic element.

The inventors have discovered that the extrachromosomal genetic element of *Plasmodium* is
25 particularly useful as a marker of *Plasmodium* infection in a human or animal subject, because the detection of said element is not subject to the disadvantages of other assay methods, in particular the prevalence of false negative detection. As a consequence, fewer numbers of *Plasmodium*-infected hosts escape detection, by screening such hosts for the presence of the extrachromosomal genetic element according to the embodiments described
30 herein (1% or less false negative detection compared to 3% or more for other methods), than

by screening for the presence of other *Plasmodium*-expressed genes or by screening for the expression products of said genes.

Furthermore, the present invention is a procedure for assaying or identifying *Plasmodium* in
5 a biological sample, preferably blood or a derivative of blood and in particular a biological sample which comprises dried blood.

The present invention clearly contemplates diagnostic assays which are capable of both genera-specific or species-specific detection. Accordingly, in one embodiment, the
10 *Plasmodium* *ssp.* extrachromosomal genetic element probe or primer or a homologue, analogue or derivative thereof comprises DNA capable of being used to detect multiple *Plasmodium* *ssp.* In an alternative embodiment, the *Plasmodium* *ssp.* extrachromosomal genetic element probe or primer or a homologue, analogue or derivative thereof comprises DNA capable of being used to detect a particular *Plasmodium* *ssp.*

15 The inventors have discovered further that the coding region of a *Plasmodium* extrachromosomal genetic element is highly-conserved in different *Plasmodium* *ssp.*, while there is much more variation at the nucleotide level in the non-coding regions. Whilst not being bound to any theory or mode of action, the more highly conserved sequences in the
20 extrachromosomal genetic element derived from a particular species of *Plasmodium* are particularly useful as genera-specific probes and/or primers for the detection of any *Plasmodium*, while the less-conserved sequences of said element may be useful as species-specific probes and/or primers for the detection of a sub-group of *Plasmodium*, for example a sub-group which infects humans or primates as opposed to other animals, or which induces
25 a specific form of malaria in humans.

The present inventors have also shown herein that certain sequences of the *Plasmodium* cytochrome *c* oxidase differ between species. Accordingly, a preferred embodiment of the present invention extends to the use of nucleotide sequences derived from the mitochondrial
30 extrachromosomal genetic element of *Plasmodium*, more preferably derived from *P.*

falciparum or *P. vivax* in the diagnosis of species-specific infections by one or more of *P. malariae*, *P. ovale*, *P. vivax* or *P. falciparum*, amongst others.

According to this embodiment, the nucleotide sequence set forth in SEQ ID NO:11 is a
5 "universal probe" for the detection of at least *P. falciparum* and *P. vivax*, whilst SEQ ID Nos:
21 and 22 are species-specific probes for the detection of *P. falciparum* and *P. vivax*,
respectively. Particularly preferred primer combinations for the species-specific detection of
P. falciparum include, but are not limited to primers comprising SEQ ID Nos:7 and 8, SEQ ID
Nos: 11 and 15, SEQ ID Nos: 11 and 16, SEQ ID Nos:11 and 17 SEQ ID Nos:16 and 18 and
10 alternative combinations thereof readily determined by those skilled in the art. Particularly
preferred primer combinations for the species-specific detection of *P. vivax* include, but are
not limited to primers comprising SEQ ID Nos:11 and 12 and SEQ ID Nos:13 and 14 and
alternative combinations thereof readily determined by those skilled in the art.

15 Furthermore, one or more of the diagnostic assays described herein may also be adapted to
a genera-specific or species-specific assay by varying the stringency of the hybridisation step.
Accordingly, a low or lower stringency hybridisation may be used to detect several different
species of *Plasmodium* in one or more biological samples being assayed, while a high or
higher stringency of hybridisation is used to detect the presence of a specific species of
20 *Plasmodium*.

For the purposes of defining the level of stringency, a low stringency is defined herein as
being a hybridisation and/or a wash carried out in 6xSSC buffer, 0.1% (w/v) SDS at 28°C.
A moderate stringency is defined herein as being a hybridisation and/or wash carried out in
25 2xSSC buffer, 0.1% (w/v) SDS at a temperature in the range 45°C to 65°C. A high
stringency is defined herein as being a hybridisation and/or wash carried out in 0.1xSSC
buffer, 0.1% (w/v) SDS at a temperature of at least 65°C. Those skilled in the art will be
aware of equivalent reaction conditions to those described herein for defining the
hybridisation stringency.

Generally, the stringency is increased by reducing the concentration of SSC buffer, and/or increasing the concentration of SDS and/or increasing the temperature of the hybridisation and/or wash. Those skilled in the art will be aware that the conditions for hybridisation and/or wash may vary depending upon the nature of the hybridisation membrane or the type of hybridisation probe used. Conditions for hybridisations and washes are well understood by one normally skilled in the art. For the purposes of clarification of the parameters affecting hybridisation between nucleic acid molecules, reference is found in pages 2.10.8 to 2.10.16. of Ausubel *et al.* (1987), which is herein incorporated by reference.

10 The detection means according to this aspect of the invention may be any nucleic acid-based detection means, for example nucleic acid hybridisation techniques or paper chromatography hybridisation assay (PACHA) or an amplification reaction such as a polymerase chain reaction (PCR) or nucleic acid sequence-based amplification (NASBA) system. The invention further encompasses the use of different assay formats of said nucleic acid-based detection
15 means, including restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), single-strand chain polymorphism (SSCP), amplification and mismatch detection (AMD), interspersed repetitive sequence polymerase chain reaction (IRS-PCR), inverse polymerase chain reaction (iPCR) and reverse transcription polymerase chain reaction (RT-PCR), amongst others.

20

Wherein the detection means is a nucleic acid hybridisation technique, the *Plasmodium* extrachromosomal genetic element probe may be labelled with a reporter molecule capable of producing an identifiable signal (e.g. a radioisotope such as ^{32}P or ^{35}S or a biotinylated molecule). According to this embodiment, those skilled in the art will be aware that the
25 detection of said reporter molecule provides for identification of the *Plasmodium* extrachromosomal genetic element probe and that, following the hybridisation reaction, the detection of the corresponding *Plasmodium ssp.* extrachromosomal genetic element in the biological sample is facilitated. Those skilled in the art will recognise that additional probes may be used to confirm the assay results obtained using a single probe.

30

A variation of the nucleic acid hybridisation technique contemplated by the present invention is the paper chromatography hybridisation assay (PACHA) described by Reinhartz *et al.* (1993) and equivalents thereof, wherein a target nucleic acid is labelled with a reporter molecule such as bitorin, applied to one end of a nitrocellulose or nylon membrane filter strip
5 and subjected to chromatography under the action of capillary or other forces (eg. an electric field) for a time and under conditions sufficient to promote migration of said target nucleic acid along the length of said membrane to a zone at which a *Plasmodium* extrachromosomal genetic element DNA probe is immobilised thereto, for example in the middle region. According to this detection format, labelled target nucleic acid comprising a *Plasmodium*
10 extrachromosomal genetic element which is complementary to the probe will hybridise thereto and become immobilised in that region of the membrane to which the probe is bound. Non-complementary sequences to the probe will diffuse past the site at which the probe is bound. Those skilled in the art will be aware that the target nucleic acid may comprise a crude or partially-pure extract of *Plasmodium* DNA or RNA or alternatively, comprise amplified DNA
15 or purified *Plasmodium* extrachromosomal genetic element DNA. Additional variations of this detection means which utilise the nucleotide sequences described herein are clearly encompassed by the present invention.

Wherein the detection means is an RFLP, nucleic acid derived from the biological sample,
20 in particular DNA, is digested with one or more restriction endonuclease enzymes and the digested DNA is subjected to electrophoresis, transferred to a solid support such as, for example, a nylon or nitrocellulose membrane, and hybridised to the *Plasmodium* extrachromosomal genetic element probe as hereinbefore defined, optionally labelled with a reporter molecule. According to this embodiment, a specific pattern of DNA fragments is
25 hybridised to the *Plasmodium* extrachromosomal genetic element probe, said pattern optionally specific for a particular *Plasmodium* *ssp.*, to enable the user to distinguish between different species of the parasite.

Wherein the detection means is an amplification reaction for example a polymerase chain
30 reaction or a nucleic acid sequence-based amplification (NASBA) system or a variant of same,

one or more nucleic acid primer molecules of at least 15 contiguous nucleotides in length derivable from the *Plasmodium* extrachromosomal genetic element as hereinbefore defined, or its complementary nucleotide sequence or a homologue, analogue or derivative thereof, is hybridised to the biological sample comprising nucleic acid or alternatively, to nucleic acid
5 derived from said sample and nucleic acid copies of the *Plasmodium* extrachromosomal genetic element present in said sample or a part or fragment thereof are enzymically-amplified.

Those skilled in the art will be aware that there must be a sufficiently high percentage
10 nucleotide sequence identity between the *Plasmodium* extrachromosomal genetic element primers and the sequences in the template molecule to which they hybridise. As stated previously, the hybridisation conditions may be varied to promote hybridisation.

Preferably, the *Plasmodium* extrachromosomal genetic element primer is at least 95%
15 identical to the complement of the nucleotide sequence in the template molecule to which it hybridises. More preferably, each *Plasmodium* extrachromosomal genetic element primer is substantially the same as the complement of the nucleotide sequence in the template molecule to which it hybridises.

20 Preferably, the *Plasmodium* extrachromosomal genetic element primer is contained in an aqueous mixture of other nucleic acid primer molecules. More preferably, the nucleic acid primer molecule is in a substantially pure form.

The *Plasmodium* extrachromosomal genetic element primer preferably comprises the sequence
25 of nucleotides set forth in any one or more of SEQ ID Nos: 5-22 or Figures 9 or 10 or a complementary strand or a homologue, analogue or derivative thereof.

In a more particularly preferred embodiment, the *Plasmodium* extrachromosomal genetic element primers are hybridised to a *Plasmodium* extrachromosomal genetic element contained
30 in the biological sample being analysed, as probe pairs, in the combinations comprising SEQ

ID Nos: 5 and 6; or SEQ ID Nos: 7 and 8; or SEQ ID Nos: 9 and 10; or SEQ ID Nos: 11 and 12; or SEQ ID Nos: 11 and 15; or SEQ ID Nos: 11 and 16; or SEQ ID Nos: 11 and 17; or SEQ ID Nos: 13 and 14; or SEQ ID Nos: 16 and 18; or SEQ ID Nos: 21 and 22 or complementary strands, homologues, analogues or derivatives thereof.

5

The present invention particularly contemplates the use of primers as set forth in any one or more of SEQ ID Nos: 11-18 as being useful in the differentiation of *Plasmodium* species as well as for detecting *Plasmodium* in a biological sample.

- 10 The *Plasmodium* extrachromosomal genetic element present in the biological sample, or a part or fragment thereof which is enzymically-amplified, is defined herein as a "template molecule". The template molecule may be a genetic sequence which is at least 40% identical at the nucleotide sequence level to SEQ ID Nos: 1-4 or to its complementary nucleotide sequence or to the *P. vivax*, *P. ovale*, *P. berghei*, *P. falciparum* or *P. malariae* sequences
15 set forth in Figure 9 or Figure 10, the only requirement being that it comprises a *Plasmodium* extrachromosomal genetic element primer as hereinbefore defined.

Those skilled in the art will also be aware that, in one format, the polymerase chain reaction
20 provides for the hybridisation of non-complementary *Plasmodium* extrachromosomal genetic element primers to different strands of the template molecule, such that the hybridised primers are positioned to facilitate the 5'-3' synthesis of nucleic acid in the intervening region, under the control of a thermostable DNA polymerase enzyme. As a consequence, the polymerase chain reaction provides an advantage over other detection means in so far as the
25 nucleotide sequence in the region between the hybridised *Plasmodium* extrachromosomal genetic element primers may be unknown and unrelated to any known nucleotide sequence.

In a particularly preferred embodiment, the nucleic acid template molecule comprises, in
30 addition to other nucleotide sequences, a sequence of nucleotides derived from or contained

within any one or more of the sequences set forth in SEQ ID Nos: 1-18 or a complementary sequence or a homologue, analogue or derivative thereof.

In an alternative embodiment, wherein the detection means is AFLP, the *Plasmodium* extrachromosomal genetic element primers are selected such that, when nucleic acid derived from the biological sample, in particular DNA, is amplified, different length amplification products are produced from different *Plasmodium ssp.* The amplification products may be subjected to electrophoresis, transferred to a solid support such as, for example, a nylon or nitrocellulose membrane, and hybridised to the *Plasmodium* extrachromosomal genetic element probe as hereinbefore defined, optionally labelled with a reporter molecule. According to this embodiment, a specific pattern of amplified DNA fragments is hybridised to the *Plasmodium* extrachromosomal genetic element probe, said pattern optionally specific for a particular *Plasmodium ssp.*, to enable the user to distinguish between different species of the parasite in much the same way as for RFLP analysis.

The technique of AMD facilitates, not only the detection of a *Plasmodium* extrachromosomal genetic element in a biological sample, but also the determination of nucleotide sequence variants which differ from the *Plasmodium* extrachromosomal genetic element primers and probes used in the assay format.

Wherein the detection means is AMD, the *Plasmodium* extrachromosomal genetic element probe is end-labelled with a suitable reporter molecule and mixed with an excess of the amplified template molecule. The mixtures are subsequently denatured and allowed to renature to form nucleic acid "probe:template hybrid molecules" or "hybrids", such that any nucleotide sequence variation between the probe and the template molecule to which it is hybridised will disrupt base-pairing in the hybrids. These regions of mismatch are sensitive to specific chemical modification using hydroxylamine (mismatched cytosine residues) or osmium tetroxide (mismatched thymidine residues), allowing subsequent cleavage of the modified site using piperidine. The cleaved nucleic acid may be analysed using denaturing polyacrylamide gel electrophoresis followed by standard nucleic acid hybridisation as

described *supra* to detect the *Plasmodium* extrachromosomal genetic element nucleotide sequences.

Those skilled in the art will be aware of the means of end-labelling a genetic probe according
5 to the performance of the invention described in this embodiment.

According to this embodiment, the use of a single end-labelled probe allows unequivocal localisation of the sequence variation. The distance between the point(s) of sequence variation and the end-label is represented by the size of the cleavage product.

10

In an alternative embodiment of AMD, the probe is labelled at both ends with a reporter molecule, to facilitate the simultaneous analysis of both DNA strands.

Wherein the detection means is IRS-PCR, the *Plasmodium* extrachromosomal genetic element
15 primers are selected such that they each include one highly-repetitive restriction enzyme cleavage site, for example *AluI*, which is ubiquitous in many genomes. According to this embodiment, the appropriate restriction enzyme cleavage site is selected such that it is ubiquitous in *Plasmodium* extrachromosomal genetic element nucleotide sequences. The amplified template DNA is electrophoresed under conditions which facilitate high resolution
20 and optionally probed with a labelled *Plasmodium* extrachromosomal genetic element probe.

Optionally, the amplified template DNA may be end-filled using Klenow fragment of DNA polymerase I or other suitable means, prior to the electrophoresis step.

25 According to this embodiment, different combinations of primers produce different patterns of amplified template nucleic acid.

Furthermore, with any primer combination used, each *Plasmodium ssp.* will produce a distinctive pattern of amplified template nucleic acid. As a consequence, the detection means
30 is suitable for distinguishing between different *Plasmodium ssp.*, in addition to being useful

for the detection of the *Plasmodium* extrachromosomal genetic element *per se* in a biological sample.

Wherein the detection means is RT-PCR, the nucleic acid sample comprises an RNA
5 molecule which is a transcription product of the *Plasmodium* extrachromosomal genetic element DNA or a homologue, analogue or derivative thereof. As a consequence, this assay format is particularly useful when it is desirable to determine expression of one or more *Plasmodium* extrachromosomal genetic element genes.

10 According to this embodiment, the RNA sample is reverse-transcribed to produce the complementary single-stranded DNA which is subsequently amplified using standard procedures.

Variations of the embodiments described herein are described in detail by McPherson *et al.*
15 (1991), which is incorporated in the references.

The present invention clearly extends to the use of any and all detection means referred to *supra* for the purposes of diagnosing *Plasmodium* infection in humans and other animals.

20 The amplification reaction detection means described *supra* may be further coupled to a classical hybridisation reaction detection means to further enhance sensitivity and specificity of the inventive method, in particular by hybridising the amplified DNA with a *Plasmodium* extrachromosomal genetic element probe which is different from any of the *Plasmodium* extrachromosomal genetic element primers used in the amplification reaction.

25

Accordingly, a particularly preferred embodiment of the inventive method comprises the further step of detecting the amplified nucleic acid by contacting one or more of the nucleotide sequences set forth in SEQ ID Nos:19-22 thereto for a time and under conditions sufficient for hybridisation to occur.

30

Similarly, the hybridisation reaction detection means described *supra* may be further coupled to a second hybridisation step employing a *Plasmodium* extrachromosomal genetic element probe which is different from the probe used in the first hybridisation reaction.

5 The nucleotide sequences set forth in SEQ ID Nos: 19-22 are particularly suited to the performance of this embodiment, however those skilled in the art would readily be able to utilise the nucleotide sequences provided by the present invention in the performance of this embodiment. In particular, SEQ ID Nos:19 and 20 enable the identification of LSU and SSU sequences, respectively in a *Plasmodium ssp.*, whilst SEQ ID Nos: 21 and 22 may be used
10 for the specific detection of amplified or hybridised *coxI* genetic sequences derived from *Plasmodium falciparum* and *P. vivax*, respectively.

A further aspect of the invention provides an isolated extrachromosomal genetic element probe or primer derived from *Plasmodium ssp.*, or a homologue, analogue or derivative
15 thereof, according to the embodiments described herein.

Preferably, the extrachromosomal genetic element probe or primer is derived from a *Plasmodium ssp.* selected from the list comprising *P. berghei*, *P. falciparum*, *P. vivax*, *P. malariae*, *P. ovale*, *P. cynomolgi*, *P. gonderi*, *P. (Hepatocytis) kochi*, *P. inui*, *P. knowlesi*,
20 *P. reichenowi*, *P. rodhaini*, *P. schwerzi*, *P. cathemerium*, *P. elongatum*, *P. relictum*, *P. lophurae*, *P. gallinaceum* or *P. yoelii*, amongst others.

In a particularly preferred embodiment, the extrachromosomal genetic element probe or primer is derived from *P. falciparum*, *P. berghei*, *P. ovale*, *P. vivax* or *P. malariae*. More
25 particularly, the extrachromosomal genetic element probe or primer comprises a sequence of nucleotides which is at least 95% identical to the sequence set forth in any one or more of SEQ ID Nos: 1-22, or any one or more of the *P. berghei*, *P. ovale*, *P. vivax* or *P. malariae* sequences set forth in Figure 9 or the *P. falciparum*, *P. ovale*, *P. vivax* or *P. malariae* sequences set forth in Figure 10 or any one or more of the sequences set forth or a
30 complementary nucleotide sequence, homologue, analogue or derivative thereof which is

at least useful as a primer or probe for the diagnosis of infection of a human or animal subject by a *Plasmodium ssp.*

Alternatively, the probe or primer at least comprises a nucleotide sequence which is capable
5 of encoding an amino acid sequence which is encoded by one or more of SEQ ID Nos:1-4 or a nucleotide sequence set forth in Figure 9 or 10 or a complementary sequence thereto.

Wherein the extrachromosomal genetic element is a plastid or plastid-like molecule, it is preferred that it be derived from a species of *Plasmodium* other than *P. falciparum*.

10

A further aspect of the present invention contemplates a kit for convenient detection of a *Plasmodium ssp.* in a biological sample.

In an alternative embodiment, the kit of the present invention is also useful for convenient assay
15 of infection by a *Plasmodium ssp.* parasite, wherein the sample being tested is derived from a human or other animal or mosquito suspected of being infected with said parasite.

The kit of the present invention is compartmentalized to contain in a first compartment, one or more nucleic acid molecules which comprise a sequence of nucleotides corresponding to a
20 *Plasmodium* extrachromosomal genetic element or a complementary nucleotide sequence or a homologue, analogue or derivative thereof as hereinbefore defined.

In a preferred embodiment, the first compartment is adapted to contain one or more nucleic acid molecules which are at least 95% identical to the nucleotide sequence set forth in any one or
25 more of SEQ ID Nos: 1-22 or any one or more of the *Plasmodium vivax*, *P. ovale*, *P. falciparum*, *P. berghei* or *P. malariae* sequences set forth in Figure 9 and/or Figure 10 or its complement or a derivative, homologue or analogue thereof. In a more preferred embodiment, the kit at least comprises one or more of the probe or primer sequences as set forth in any one of SEQ ID Nos: 5-22. The selection of SEQ ID Nos:21 and/or 22 as a probe is particularly
30 suited to species-specific detection assay formats.

In a particularly preferred embodiment, the subject kit comprises a first primer and a second primer for the amplification of nucleic acid derived from or related to a *Plasmodium* extrachromosomal genetic element, such as a mitochondrion or plastid-like element. According to this embodiment, the first primer preferably comprises a sequence selected from
5 SEQ ID Nos: 5, 7, 9, 11, 14 or 18 and the second primer preferably comprises a sequence selected from SEQ ID Nos: 6, 8, 10, 12, 13 or 15-17 or a derivative thereof.

In a more particularly preferred embodiment, the first and second primers comprise the sequences set forth in SEQ ID Nos: 5 and 6, or SEQ ID Nos: 11 and 12 or SEQ ID Nos: 11 and
10 15 or SEQ ID Nos: 11 and 16 or SEQ ID Nos: 11 and 17 or SEQ ID Nos: 13 and 14 or SEQ ID Nos: 16 and 18, respectively. These combinations are particularly suited to species-specific detection assay formats.

The invention clearly extends to kits at least comprising one or more pairs of said primers.
15

The invention extends further to such kits wherein both primers of a primer pair are provided in the same compartment, in aqueous solution or dried, such that the subject primers are at a relative concentration suitable for subsequent use in an amplification reaction.

20 The kit optionally comprises several second containers comprising a reaction buffer suitable for use in one or more of the detection means described herein and optionally several third containers comprising a nucleic acid molecule positive standard, to which the assay sample result may be compared.

25 In an exemplified use of the subject kit, a negative control reaction is carried out in which the contents of the first container are contacted with the contents of the second container. At the same time, the sample to be tested is contacted with the contents of the first and second containers for a time and under conditions sufficient for hybridisation to occur. If the reagents contained in the first container provided are not labelled with a reporter molecule, then the
30 contents of the first container may be so labelled prior to the hybridisation reaction being carried

out. The hybridised test sample and the negative control sample are then subjected to a detecting means as hereinbefore described. In analysing the results obtained using said kit, the control negative control reaction, test sample and nucleic acid molecule positive standard are compared side-by-side. The contents of the third container should always provide a positive
5 result upon which to compare the results obtained for the negative control and test sample. If the results of the test sample are identical to the results obtained for the negative control, then the biological sample does not contain a *Plasmodium ssp.* extrachromosomal genetic element. However, if the test sample produces a nucleic acid molecule which is similar or the same as that contained in the positive standard, albeit of different intensity, then the biological sample
10 contains a *Plasmodium ssp.* extrachromosomal genetic element.

The kit may further comprise additional probes and/or primers for the purpose of detecting amplified or hybridised nucleic acid in additional rounds of hybridisation and/or
15 amplification.

The present invention is further described by the following non-limiting Examples.

EXAMPLE 1

20 Preparation of *Plasmodium berghei* extrachromosomal DNA

Plasmodium berghei (ANKA strain) was maintained in Swiss White mice by continuous blood passage. Development of parasitemia was monitored daily by thin blood film analysis (Shute, 1988). Parasites were obtained by lysis of infected red blood cells with 1% saponin. The extrachromosomal element was purified from the parasites using a modified procedure
25 of the Qiagen plasmid mini preparation kit (Qiagen Inc., Chatsworths, CA, USA). Parasites from 10 infected mice (20-25 g) with a parasitemia of 60% were resuspended in 5 ml of P1 buffer, lysed with 5 ml of P2 buffer and neutralised with 5 ml of P3 buffer. After chilling on ice for 20 minutes, the precipitate was removed by centrifugation according to the manufacturer's recommendation and 200 μ l of proteinase K (50 mg/ml) were added to the
30 supernatant, which was then reincubated for 2 hours at 37 C. The supernatant was

subsequently passed through a tip-20 Qiagen column which had previously been equilibrated with 1 ml of QBT buffer. The column was washed four times with 1 ml of QC buffer each. Finally, the extrachromosomal element was eluted with 1 ml of QF - buffer which was preheated to 65 C. The DNA was precipitated with isopropanol, washed with 70% ethanol, dried and dissolved in 25 μ L of TE buffer.

EXAMPLE 2

Preparation and restriction digest of *P. berghei* extrachromosomal DNA

- 10 *Plasmodium berghei* extrachromosomal DNA was extracted from the parasite using the Qiagen plasmid mini preparation kit (Qiagen Inc., Chatsworths, CA, USA). Electron microscopic analysis of this preparation showed circular DNA elements of about 10 times the size of control pBR 322 plasmids (Figure 1). The preparation was not homogenous and, in addition to the circular elements many linear molecules of different lengths were observed.
- 15 The preparation is enriched for the extrachromosomal DNA elements of both circular and linear DNA representing the homologues of the 35 kb circle and 6 kb mitochondrial DNA. These are likely to be 6 kb DNA molecules which are tandemly arrayed in head-to-tail configurations.
- 20 The extracted plastid DNA was digested into 3 fragments of 15 kb (E3), 10 kb (E2) and 5.7 kb (E1) by *EcoRI* (Figure 2a). This gives the plastid an estimated size of 31 kb. *Hind III* digest of the DNA yielded 6 fragments of 22.4 kb (H6), 4.4 kb (H5), 1.85 kb (H4), 1.23 kb (H3), 0.95 kb (H2) and 0.7 kb (H1), respectively (Figure 2b). H3 and H5 are fragments from the mitochondrial 6 kb genome.
- 25 The estimated size of the *P. berghei* circle is 31 kb according to Electron microscopic measurements using pBR322 as control as well as from size calculations using the *EcoR I* restriction digest fragments.

- 30 Extrachromosomal circular DNA has not only been found in *Plasmodium* species but also in

other parasitic protozoa such as *Babesia* and *Entamoeba* (Gozar and Bagnara, 1995; Egea and Lang-Unnasch, 1995; Sehgal et al., 1994) suggesting a common evolutionary origin of this circular DNA material (Williamson et al. 1994). By maintaining such extrachromosomal information during evolution it appears that this highly conserved and seemingly functional
5 extrachromosomal DNA molecule is important for parasite development and that knowledge of its functions will greatly aid in providing novel targets for drug development.

Our preliminary tests using an antisense oligonucleotide approach indicate that this extrachromosomal element may indeed be crucial for parasite survival.

10

EXAMPLE 3

PCR amplification and sequence analysis of plastid DNA.

In order to obtain a genetic map of the approximately 35 kb *Plasmodium berghei* extrachromosomal plastid, polymerase chain reaction (PCR) amplifications and sequence
15 analysis of plastid DNA were carried out.

PCR was performed using the United States Biochemical (Amersham) PCR kit in a 100 μ l reaction mixture containing 2 mM $MgCl_2$, 0.2 mM of each dNTP, 4 ng/ μ L of each primer, 5 units of *Taq* DNA polymerase, 10 μ L of the 10 X PCR buffer and 1 μ L of the
20 extrachromosomal DNA prepared as described in Examples 1 and 2. A "hot start" was carried out at 95°C for 5 minutes without the dNTPs and *Taq* polymerase. This was followed by the addition of dNTPs and *Taq* polymerase and 40 cycles of denaturation (90°C, 1.5 minutes), annealing (55°C, 3 minutes) and extension (72°C, 5 minutes). A final extension was performed at 72°C for 10 minutes.

25

The PCR products were loaded onto a 1 % low melting point agarose gel, extracted by the freeze-thaw method (Shoemaker and Salyers, 1990) and then cloned into the Promega pGEM-T vector.

30 Clone H2a was constructed by cloning the second fragment of a *Hind*III digest of the

extrachromosomal element into the pBluescript vector. (Stratagene, USA).

The clones were sequenced using the ABI PRISM Dye terminator cycle sequencing kit from Perkin-Elmer on the 373A DNA sequencer from Applied Biosystems. The percentage
5 homology with the *P. falciparum* extrachromosomal element (Accession No. X 95275 and X 95276) was obtained using the Martinez/Needleman-Wunsch DNA alignment programme from DNASTAR.

- PCR amplification of different parts of the extrachromosomal plasmid were performed using
10 primer sets homologous to sequences from the 35 kb circle of *P. falciparum* (Table 1). These include the primer sets comprising SEQ ID Nos: 5 and 6 (L/L Primer set), SEQ ID Nos: 7 and 8 (L/S primer pair) and SEQ ID Nos: 9 and 10 (S/S Primer pair, homologous to the small-subunit (ssu) -rRNA of *P. falciparum*).
- 15 The amplified regions obtained with these primers lay within the large subunit (lsu) -rRNA gene, *rpo B* gene, the cluster of 10 tRNAs, part of the cluster of four tRNAs located close to the 3' end of the *tufA* gene in *P. falciparum* as well as the region between the *lsu*-rRNA and the *ssu*-rRNA genes.
- 20 All PCR fragments were cloned into the pGem-T vector from Promega. Sequence analysis performed using the Martinez/Needleman-Wunsch DNA alignment on all clones which had been purified using Qiagen midi plasmid preparation columns showed a similarity index of greater than 80% with the *P. falciparum* circle except for the PPH and PWQ fragment (Table
1). The PRB fragment was homologous to the *P. falciparum* *rpo B* gene with a similarity
25 index of 87.9% for the DNA sequence and 85.6% for the corresponding amino acid sequence (using the Lipman-Pearson protein alignment). The PPH sequence spanning the cluster of 10 tRNA genes had a similarity index of only 78%. While the tRNA coding regions were highly similar to those in *P. falciparum* the non-coding spaces were much less conserved between the two Plasmodium species.

In order to examine if the *lsu-rRNA* gene in *P. berghei* exists as a repeat, a single forward primer (L3) homologous to the 3' end of the *P. falciparum* *lsu-rRNA* sequence and 2 distinct reverse primers homologous to the ORF 470 (04) and the start of the cluster of 10 *tRNA* genes (3H) of the *P. falciparum* circle were designed. The fragment amplified with the L3/04 primer set (PL470) was distinct from that amplified using the L3/3H set (PLH). Sequence analysis of PL470 showed a homology of 83 % with the same region in *P. falciparum*. The sequence of PLH was homologous to the 3' end of the *lsu-rRNA* and the 3' end of *rps 4* of the *P. falciparum* circle (data not shown) indicating that the *lsu-rRNA* gene exists as a repeat in *P. berghei*. In addition, a cluster of intervening *tRNA* genes was present between the *lsu-rRNA* and *ssu-rRNA* genes (fragment PLS). This repetition and arrangement is similar to the organisation of the *P. falciparum* circle, where a palindromic sequence of genes for the subunit *rRNAs* and several *tRNAs* exists. Each arm of the palindrome contains one *ssu* and one *lsu-rRNA* gene and a cluster of intervening *tRNA* genes (Gardner *et al.*, 1993).

From the nucleotide sequences set forth in SEQ ID Nos: 1-4, it is clear that the genes in the *P. berghei* circle are homologous to those in the 35 kb *P. falciparum* circle. Major differences in sequence are observed in the non-coding spaces between *tRNA* gene clusters. The arrangement of genes appears to be similar in both *Plasmodium* species and a repeat of the *rRNA* genes does not only exist in *P. falciparum* but also in the *P. berghei* circle.

EXAMPLE 4

Southern Hybridisation of restriction fragments

Fragments from the *Hind*III and *Hind*III/ *Eco*RI digests of the *Plasmodium berghei* extrachromosomal element were separated on a 1 % (w/v) agarose gel at 120 V for 4 hours. The separated fragments were then transferred onto a Nylon membrane (Hybond-N, Amersham) by capillary action using 20x SSC buffer (0.3M sodium citrate, 3M sodium chloride, pH 7.0). Southern hybridization was performed using probes specific for the approximately 35 kb circle that were made from the cloned PCR products, according to the preceding Examples.

The PCR products were liberated from the vector by digestion with *ApaI* and *PstI*. The enhanced chemiluminescence (ECL) direct nucleic acid labelling and detection system (Amersham International PLC, England) was used for labelling the probe, for hybridisation and for detection.

5

Each of these steps were carried out according to the manufacturer's instruction. First, 8 μ g of probe in a volume of 20 μ L were denatured by boiling for 5 minutes and immediately cooled on ice for 5 minutes. 20 μ L of labelling reagent were then added. This was followed by the addition of 20 μ L of glutaraldehyde solution. The mixture was incubated for 20 minutes at 37°C before addition to the hybridization buffer. The ECL Gold hybridisation buffer containing 0.5M NaCl and 5% blocking agent was used for hybridisation. The blots were prehybridised for 2 hours at 42°C and the labelled probe was added to a final concentration of 800 ng DNA/ml. Hybridisation was allowed to proceed overnight at 42°C. The blots were washed twice in primary wash buffer containing 6M urea, 0.4% SDS and 0.5x SSC at 42°C for 20 minutes. This was followed by two rounds of washing in 2x SSC buffer at room temperature for 10 minutes. For detection, 6.5 ml of equal volumes of detection reagents 1 and 2 were mixed and added to the blot for 1 minute. The blot was then drained, wrapped in Saran Wrap and the DNA side was exposed to an autoradiography film.

20 A double digest of the *P. berghei* circle with *HindIII* followed by *EcoRI* resulted in the following fragments: 10kb (E2), 5.7kb (E1), 5.0kb (HE2), 4.4kb (H5), 2.3kb (HE1), 1.85 (H4), 1.23 (H3), 0.95(H2) and 0.7kb (H1). The PS 1 probe hybridised to H2, the PL470 probe hybridised to H6 and HE2 while the PWQ probe hybridised to H6 and E2 (Fig. 3).

25 The results obtained with various other probes are shown in Table 2. Of interest to note is that H2 contained 2 distinct fragments which hybridised with PS 1 and PL3. One of the H2 fragments (H2a) was cloned into Bluescript vector (pBS KS (II)+) and sequenced. The sequence corresponded to the internal region of the *P. falciparum* 35 kb ssu-rRNA gene (Table 1, sequence H2a). The other fragment (H2b) arose from the two Hind III sites within the
30 lsu-rRNA gene. The presence of these two sites was confirmed by the sequences from the

Table 1. Description of clones of various segments from the extrachromosomal element in *P. berghei* and their percentage homology with *P. falciparum*.

	Name of clone	Description	Size (bp)	Percentage homology with <i>P. falciparum</i>	<i>EcoRI/HindIII</i> sites
5	H2a	Second fragment of <i>HindIII</i> digest containing SSU rRNA	949	92.3	Two <i>HindIII</i> sites
	PS1	PCR product of SSU rRNA	526	94.3	Nil
	PL1	PCR product of LSU rRNA	595	95.5	One <i>HindIII</i> site
	PL2	PCR product of LSU rRNA	595	93.8	One <i>HindIII</i> site
10	PL3	PCR product of LSU rRNA	735	88.8	One <i>HindIII</i> site
	PLS	PCR product of tRNAs between LSU and SSU rRNA	973	87.3	Nil
	PPH	PCR product of tRNAs before the repeat	1000	78.0	One <i>EcoRI</i> site
	PLH	PCR product from LSU rRNA to His-tRNA	1118	82.3	Nil
	PL470	PCR product from LSU to ORF470	1125	83.0	Nil
15	PRB	PCR product of the RpoB gene	516	87.9	One <i>EcoRI</i> site
	PWQ	PCR product of the Phe-tRNA	161	69.6	Nil
	PB-1	Sequence derived from clones spanning the Ile-tRNA, the ssu-rRNA, the lsu-rRNA and the ORF-470 genes	5849	88.5	4 <i>Hind III</i> sites
	PB-2	Sequence derives from clones spanning the regions within the lsu-rRNA, the rps 4 and the cluster of 10 tRNA genes	2621	80.2	1 <i>Hind III</i> site and 1 <i>Eco RI</i> site

Table 2. Southern analysis of restriction digests.

5	Probe	<i>Hind</i> III digest	<i>Hind</i> III/ <i>Eco</i> RI digest	<i>Eco</i> RI digest
10	PS1	H2	H2	N.D.
	PLS	H4	H4	N.D.
	PWQ	H6	E2	E2
15	PL1	H6	HE2	N.D.
	PL2	H6	HE1, HE2	N.D.
20	PL3	H2, H4	H2, H4	E3
	PRB	H6	HE2	E2, E3
	PL470	H6	HE2	E3
25	PPH	H6	HE1	E3
	PB6K-4	H3, H5	H3, H5	N.D.
30				

PL2 and PL3 PCR products. In addition, both the H5 and the H3 fragments hybridised with probes corresponding to the *P. berghei* 6 kb mitochondrial DNA. This was not unexpected as the preparation was found to contain linear molecules as shown by electron microscopy (Fig. 1).

5

EXAMPLE 5

Physical and genetic map of the *P. berghei* 35 kb circle

A map of the approximately 35 kb *P. berghei* extrachromosomal circle was constructed based on the information from the restriction digests, Southern hybridisation experiments and the
10 sequence analysis of the PCR fragments (Figure 4a). The PPH and PRB fragments each contained an *EcoR* I restriction site (Table 1). The three *EcoR* I and six *Hind* III fragments were arranged according to their hybridisation patterns. The PRB probe hybridised to both the E2 and E3 fragments from the *EcoR* I digest indicating that E2 is positioned next to E3 (Table 2).

15

The HE2 fragment obtained from the double digest with *EcoR* I and *Hind* III, hybridised to probes PRB, PL470 and PL2 while H2b and H4 hybridised to probe PL3. Both the PL2 and PL3 fragments are regions within the *lsu-rRNA* gene, whereas the PL470 fragment contains 3' end of the *lsu-rRNA* gene. Thus, the ORF470 must be located next to the PL2 fragment.
20 H2b is situated between HE2 and H4 since H4 also hybridised with the PLS probe which contains the 5' ends of both the small and large subunits rRNA genes. H2a hybridised with probe PS 1 which corresponds to a region within the *ssu-rRNA* gene, therefore H2a must be located next to H4. Finally, HE1 is placed next to E1 as HE1 hybridised to probes PPH, PLH and PL2.

25

The arrangement of genes on the *P. berghei* circle spanning the *rpo B* gene and the cluster of 10 *tRNAs* genes is thus very similar to that of the *P. falciparum* 35 kb circle (Figure 4b). The *P. berghei* circle encodes organelle-like rRNAs, tRNAs, ribosomal proteins and RNA polymerase subunits, similar to those identified for *P. falciparum* (Preiser *et al.*, 1995).

30

EXAMPLE 6

Reverse transcription-PCR of LSU-rRNA and SSU-rRNA

In order to determine if the approximately 35 kb *Plasmodium berghei* extrachromosomal genetic element is transcriptionally active, total RNA from *P. berghei* was isolated using the RNeasy total RNA kit (Qiagen Inc., Chatsworth, CA, USA) and a combined reverse transcription - PCR (RT-PCR) reaction was carried out to amplify *lsu-rRNA* or *ssu-rRNA* transcripts.

Total RNA was isolated from *Plasmodium berghei* using the Qiagen RNeasy Total RNA kit (Qiagen Inc., Chatsworth, CA, USA). Parasites from 10 infected mice with a parasitemia of 60% were resuspended in 350 μ l of lysis buffer RLT and homogenised using a QIAshredder (Qiagen Inc.). The homogenate was cleared of insoluble material by centrifugation and 1 volume of 70% ethanol was added. The entire sample was then added to the RNeasy spin column and washed with RW1 buffer followed by two washes with RPE buffer. The RNA was eluted out with 35 μ l of water. 5 μ l of the RNA was used as starting material for the Access RT-PCR system (Promega, Madison, USA). Two primer sets, L/L (SEQ ID Nos: 5 and 6) and S/S (SEQ ID Nos: 9 and 10) were used. The manufacturer's protocol was followed with the exception of the annealing step for PCR amplification. Annealing was allowed to proceed at 55°C for 1 minute. The PCR products were separated on a 1% (w/v) agarose gel and visualised by ethidium bromide staining.

Amplification using the RT-PCR kit from Promega and a set of primers homologous to the *ssu-rRNA* produced a 526 bp fragment while amplification using a set of *lsu-rRNA* specific primers resulted in a 594bp fragment (Fig. 5).

EXAMPLE 7

Assay of blood samples for the presence of *Plasmodium ssp.*

A total of 482 *Plasmodium*-infected blood samples from four different locations, Singapore, Laos, Pakistan, India and Colombia and a defined number of negative control

blood samples, were analysed for the presence of *Plasmodium* extrachromosomal genetic elements, using the polymerase chain reaction.

Briefly, 10-100 μ L of whole patient blood (either peripheral blood from a finger prick sample or venal blood) was spotted onto a filter disc or equivalent solid support and directly amplified, using each of the primer pairs:

L/L PRIMER PAIR:

SEQ ID NO:5: 5'-GACCTGCATGAAAGATG-3'
10 SEQ ID NO:6: 5'-GTATCGCTTTAATAGGCG-3'

L/S PRIMER PAIR:

SEQ ID NO:7: 5'-GCCACTACTATGAAAATC-3'
15 SEQ ID NO:8: 5'-GCGTTCATTCTGAGCTAG-3'

S/S PRIMER PAIR:

SEQ ID NO:9: 5'-GCGGTAATACAGAAAATGCAAGCG-3'
20 SEQ ID NO:10: 5'-AGCACGAAGTACGACAGCCATGCAC-3'

20 PCR Buffer used in the amplification reactions comprised the following:

70mM Tris. pH8.8
20mM Ammonium sulphate
1 mM DTT
0.1 μ g/ μ L BSA (or 0.01 % geletin)
25 2.5mM MgCl₂

Each 100 μ L reaction included 0.4 μ g of each primer, 0.8mM dNTP mixture and 5U of *TaqI* polymerase.

30 The template DNA was fixed with methanol for 5 mins. A "hot start" was carried out at 95°C for 5 minutes without the dNTPs and *Taq* polymerase. This was followed by the addition of

dNTPs and Taq polymerase and 40 cycles of denaturation (90°C, 1.0 mins), annealing (56°C, 2 mins) and extension (72°C, 1 min). The PCR products were analysed by agarose gel electrophoresis.

- 5 The results are shown in Tables 3 and 4. The L/L primer set was capable of identifying *Plasmodium falciparum*, *P. vivax*, *P. ovale* and *P. malariae* in 100% of cases, suggesting that this primer pair is useful in the genera-specific diagnosis of *Plasmodium* infection. The S/S primer set was capable of efficiently diagnosing *P. falciparum* and *P. malariae* in 100% of cases. In marked contrast, the L/S primer set resulted in only poor diagnosis of *P. vivax* and
- 10 *P. malariae*, however detected the presence of *P. falciparum* in blood samples, suggesting that this primer pair is species-specific. The human actin primer set AC1/2 were used as positive controls.

Results also indicate that the selection of primer pairs in the diagnostic assay was of primary

15 importance in determining the reliability of the assay in diagnosing infection by *Plasmodium* *ssp.*

TABLE 3
Number and origin of *Plasmodium* infected samples

20

Origin	Number	P.fal	P.viv	P.mal	P.ova	Mixed	Controls
Singapore	74	15	26	2	2	3	26
Laos	16	15	1	-	-	-	-
25 Pakistan	68	14	53	-	-	-	1
India	11	1	10	-	-	-	-
Colombia	313	1	29	-	-	-	283
Total	482	46	119	2	2	3	310

30

TABLE 4
PCR results using the primer pairs L/L, L/S, S/S and AC1/2

Species	L/L	L/S	S/S	AC1/2
5 P.fal	46/46 (100%)	14/20 (70%)	21/21 (100%)	nd
P.viv	119/119 (100%)	6/58 (10%)	48/57 (84%)	nd
P.mal	2/2 (100%)	0/1 (0%)	1/1 (100%)	nd
P.ova	2/2 (100%)	nd	nd	nd
10 mixed	3/3 (100%)	nd	nd	nd
controls	0/310 (0%)	nd	nd	92/92 (100%)

nd = not done

EXAMPLE 8

Direct PCR amplification of extrachromosomal *Plasmodium*

DNA from dried blood spots

1. Specimen Collection

Blood was collected by fingerprick (5-10 μ l) or by venipuncture from subjects with Giemsa
 20 smear-positive *Plasmodium falciparum*, *Plasmodium vivax* and *Plasmodium malariae* malaria
 as well as from healthy controls, and spotted in replicates onto Whatman filter paper.
Plasmodium berghei (ANKA) infected mouse blood (5 μ l) was collected from the tail.
Plasmodium berghei infections were maintained by serial blood passage of 10⁷ parasites.
 Dried blood spots were placed individually into 200 μ l PCR tubes and fixed with the addition
 25 of methanol for 5 minutes. The methanol was poured off and the blood spot was dried
 thoroughly prior to PCR amplification.

2. PCR amplification

Amplification was carried out as previously described (Long *et al*, 1995) with some
 30 modifications. Each 100 μ l reaction mixture contained 1xPCR buffer (70 mM Tris, pH 8.8,
 20 mM (NH₄)₂SO₄, 1 mM DTT, 0.1 μ g/ μ l BSA) 2.5 mM MgCl₂, 0.4 μ g of each primer, 5

units of Taq DNA polymerase (Amersham) and 0.2 mM of each dNTPs. Reaction tubes were overlaid with one drop of mineral oil. The reaction was soaked at 95°C for 5 minutes then held at 80°C prior to the addition of Taq DNA polymerase and dNTPs. Amplification involved 40 cycles of 1 minute denaturation at 90°C, 2 minute annealing at 52°C and 3 minutes primer extension at 72°C. A 5 minute primer extension at 72°C was included following the final cycle.

3. *Sequences of primers.*

The primers used for amplifying the LSU-rRNA gene were as follows:

- 10 L1 5' GAC CTG CAT GAA AGA TG 3' (SEQ ID NO: 5); and
L2 5'GTA TCG CTT TAA TAG GCG 3' (SEQ ID NO: 6).

A second set of primers were designed to amplify the dihydrofolate reductase-thymidylate synthase (DHFR-TS) gene from *P.berghei* genomic DNA in control experiments:

- 15 DHFR1 5' GCA ATA TGT GCA TGT TGT AAA 3'; and
DHFR2 5'ATT CTT TAT AAA CAG ACG 3'.

The primers used for amplifying the human β -actin gene were as follows:

- AC1 5' GGG CGA CGA GGC CCA GAG C 3';
20 AC2 5' GCA TCC TGT CGG CAA TGC C 3';
AC3 5' AAG GAG AAG CTG TGC TAC 3'; and
AC4 5' TCA TGA TGG AGT TGA AG 3'.

4. *Agarose gel electrophoresis*

- 25 10 μ l of each PCR product was resolved in 1% agarose gels with TAE electrophoresis buffer (40mM Tris-acetate and 1mM EDTA, pH 8.0). Electrophoresis was carried out at 100V for 1.5 hours and the fragments were visualized under UV.

5. *DNA sequencing protocol*

- 30 The PCR products were loaded onto a 1% (w/v) low-melting point agarose gel and extracted

by the freeze-thaw method (Shoemaker and Salyers, 1990). They were then cloned into the pGEM-T vector (Promega). The clones were sequenced using the ABI PRISM Dye terminator cycle sequencing kit (Perkin Elmer) on the 373 DNA sequencer from Applied Biosystems. Multiple sequence alignment using the cluster method was carried out with the
5 DNASTAR programme.

6. Results

6.1 Detection of *P.berghei* infection in blood spots

Conditions for the PCR amplification of *P.berghei* infected mouse blood spotted on filter
10 paper were optimised using DHFR1 and DHFR2 primers. Once these conditions were established, the sensitivity of the LSU-rRNA primer set was compared with that of the DHFR-TS primer set. The LSU-rRNA primer set was designed to amplify a 594bp fragment from the *P.berghei* circular DNA while the DHFR-TS primer set amplified a 511bp fragment from *P.berghei* genomic DNA. Blood spots were prepared daily for 5 days from a mouse
15 which was initially infected with 5×10^4 parasites. Giemsa staining of thin blood films from the same animal was done daily. The LSU-rRNA primer set was more sensitive than the DHFR-TS primer set in detecting parasite DNA. The amplified LSU-rRNA fragment was detectable by ethidium bromide staining one day after infection (Figure 6a) while the DHFR-TS PCR product was only visible two days post-infection (Figure 6b). At these two time
20 points, no parasite was detected on the corresponding Giemsa-stained blood films. Parasites were only observed on the film three days post-infection.

6.2 PCR amplification of blood spots from malaria infected patients.

The above PCR amplification protocol was also applied to blood spots from 31 malaria-
25 infected patients. 15 of these samples were obtained from patients admitted to the National University Hospital in Singapore. Of these, 7 had *P.falciparum* infection, 1 had *P.malariae* and the remaining had *P.vivax* as determined by Giemsa and Quantitative Buffy Coat (QBC) diagnosis. All samples were positive for amplification with LSU primers (data not shown).

The other 16 samples were from patients in Laos with 15 *P.falciparum* infections and one
30 *P.vivax* malaria infection as determined by Giemsa diagnosis. LSU-rRNA PCR

amplifications were positive for all 16 specimens. As shown in Figure 7, the PCR products from 11 of the 16 Laotian specimens. Eight healthy persons and total DNA from two human carcinoma cell lines, CaSki and HeLa were used as controls. These were all negative when using the LSU-rRNA primer set for PCR amplification but were all positive for human β -actin (Figure 8, compare panels a and b).

EXAMPLE 9

Sequence alignment of LSU-rRNA extrachromosomal DNA from various *Plasmodium* species

10 The LSU-rRNA fragments amplified from the blood spots as described in Example 8 were cloned into the pGEM-T vector and sequenced. In addition to amplified products from the Singaporean and Laotian patients, we also amplified and sequenced LSU-rRNA fragments from Indian, Colombian and Pakistani patients. The published *P.falciparum* sequence (C10 strain) was used as the basis for all alignments and comparisons.

15

Comparison of the *Plasmodium* species used in this study showed that this region of the LSU-rRNA gene is highly conserved and the similarity between *P.falciparum*, *P.vivax*, *P.malariae*, *P. ovale* and *P.berghei* is greater than 91% (Table 5). The similarity between the C10 and other *P.falciparum* sequences ranged from 98.3%-99.8%, while that between
20 the C10 and the *P.vivax* sequences ranged from 91.1- 99.7%. The greatest divergence in sequence was observed from the *P.vivax* specimens from Pakistan and Colombia. In all cases, divergence in sequence was due to 1 or 2 base changes in isolated regions within the LSU-rRNA fragment (Figure 9).

25

TABLE 5
Percent homology of LSU-rRNA sequences with *P. falciparum*
(C10 strain) sequence

5		Name of sequence ¹	Similarity Index to Pf(C10) ²
		Pf10/P	98.3
		Pf11/P	98.5
		Pf19/I	99.7
		Pf20/L	99.7
10		Pf18/S	99.8
		Pv12/P	93.4
		Pv13/P	92.9
		Pv15/I	99.5
15		Pv16/L	99.7
		Pv17/S	93.4
		Pv86/C	91.1
		Pm1/S	93.2
		Pm38/S	92.9
20		Po35/S	93.4
		Po36/S	93.2
		Pb(ANKA)	94.2

¹ Pf denotes *P. falciparum*, Pv denotes *P. vivax*, Pm denotes *P. malariae* and Pb denotes *P. berghei*. The alphabet at the end of each name indicates the origin of the specimen; P=Pakistan, I=India, L=Laos, C=Colombian and S=Singapore. The GenBank accession numbers for Pf(C10) and Pb(ANKA) are X95275 and U79731 respectively.

² Similarity index obtained using the Martinez-Needleman-Wunsch DNA alignment programme.

EXAMPLE 10

Discussion

In this study, we have shown that it is possible to amplify the extrachromosomal circular plastid-like DNA found in *Plasmodium ssp.* This has allowed us to proceed with
5 characterising the LSU-rRNA gene from the circular DNA of malaria-infected patients using only a small volume of blood spotted on filter paper.

We have designed a pair of primers based on the sequences from *P.falciparum* and *P.berghei* such that the primers are completely homologous for both species. Using these primers, we
10 have been able to amplify the corresponding LSU-rRNA fragment from *P.falciparum*, *P.vivax*, *P.malariae* and *P.berghei* infected blood. Sequence analysis of these fragments indicates that this region of the LSU-rRNA is highly conserved between different species of *Plasmodium*. In addition, different geographic isolates of *P.falciparum* and *P.vivax* from Asia do not show distinct variations for the LSU-rRNA fragment. GenBank searches indicate
15 that this fragment sequence is unique.

The high homology between the various *Plasmodium* species has led us to examine if the LSU-rRNA specific primers are useful for the detection of malaria infections. Using *P.berghei*, the LSU-rRNA primer set was shown to be more sensitive than the DHFR primer
20 set in parasite detection in mouse blood spots. All 31 patient blood spots tested were positive regardless of the *Plasmodium* species involved while none from healthy persons was positive. These results indicate that the LSU-rRNA primers may be useful for the diagnosis of malaria infection.

25 The ease of direct PCR amplification of extrachromosomal *Plasmodium* circular DNA from dried blood spots has provided us with the means to study and characterise the genes present on this DNA molecule. To date, none of the genes on the circular DNA of *P.vivax* and *P.malariae* has been described. This is the first description of an analysis of the LSU-rRNA gene from different field isolates of *P. ovale*, *P.vivax*, *P.malariae* and *P.falciparum*. More
30 investigations are being carried out to determine the extent of sequence conservation and

arrangement of the genes on the circular DNA from different *Plasmodium* species.

EXAMPLE 11

PCR amplification and sequence analysis of cox I gene

5 To obtain the complete sequence of the mitochondrial cox I gene, a set of primers was designed based on the published *P. falciparum* sequence (GenBank accession number M76611). PCR using this primer set with blood spots from *P. vivax* infected patients resulted in fragments of 1.5kb in size (Figure 10). These were cloned into pGEM-T vector (Promega). The clones were sequenced in both directions using the ABI PRISM dye terminator cycle sequencing kit on the
10 374 DNA sequencer from Applied Biosystems. DNA sequence alignments were carried out using the Martinez/Needleman-Wunsch DNA alignment. The DNA sequences from 4 different *P. vivax* isolates were highly conserved (greater than 99% similarity). However, these sequences were less homologous (83%) when compared with the corresponding cox I gene from *P. falciparum*.

15

EXAMPLE 12

Plasmodium species identification in blood samples

In order to differentiate between *P. vivax* and *P. falciparum* infection, two sets of *P. vivax* specific
20 primers (PV1 - SEQ ID No: 12 and P2 - SEQ ID No: 11; PV2 - SEQ ID No: 13 and P3 - SEQ ID No: 14) and four sets of *P. falciparum* specific primers (PF1 - SEQ ID No: 15 and P2 - SEQ ID NO 11; PF2 - SEQ ID No: 16 and P2 - SEQ ID No: 11; PF3 - SEQ ID No: 17 and P2 - SEQ ID NO 11; PF2 - SEQ ID No: 16 and P4 - SEQ ID No: 18) were designed based on the mitochondrial cox I genes of the two species. PCR assays were carried out on whole patient's
25 blood spotted onto a filter disc as described for Example 7. The PCR products were analysed by agarose gel electrophoresis.

The results are shown in Tables 6, 7, 8 and 9. The three sets of *P. falciparum* specific primers only detected *P. falciparum* infected blood but not the other three human *Plasmodium* species.
30 The *P. vivax* specific primers (PV1/P2) detected only 92% of the *P. vivax* infected blood and a

false positive with *P.malariae* was also observed. This primer set does not react with *P.falciparum* or *P.ovale* (Table 6).

TABLE 6

Results using Plasmodium species specific primer set PF1/P2 and PV1/P2

Species	<i>P.falciparum</i> primer set I (PF1/P2)	<i>P.vivax</i> primer set I (PV1/P2)
P.fal	12/12	0/12
P.viv	0/26	24/26
P.mal	0/2	1/2
P.ova	0/2	0/2
Pm/Pf	1/1	0/1
Pv/Pf	2/2	2/2
Controls	0/7	0/7

TABLE 7

Results using Plasmodium species specific primer set PF2/P2

Species	<i>P.falciparum</i> primer set II (PF2/P2)
P.fal	6/6
P.viv	0/14
P.mal	0/2
P.ova	0/2
Controls	0/7

TABLE 8
Results using Plasmodium species specific primer set PF3/P2

Species	<i>P. falciparum</i> primer set III (PF3/P2)
P.fal	9/9
P.viv	0/12
P.mal	0/2
P.ova	0/2
Controls	0/7

TABLE 9
Results using Plasmodium species specific primer sets PF2/P4 and PV2/P3

Species	<i>P. falciparum</i> primer set IV (PF2/P4)	<i>P. vivax</i> primer set II (PV2/P3)
P.fal	20/20	0/20
P.viv	0/31	31/31
Pv/Pf	3/3	3/3
Pm/Pf	2/2	0/2
Pv/Po	0/3	3/3
Controls	0/10	0/10

EXAMPLE 13

Sensitivity of PCR assay for Plasmodium species in blood samples

The minimum number of parasites detectable by PCR assay was determined by using 1 µl of whole patient blood or diluted blood spotted on filter disc. Using the L/L (SEQ ID NOS 5 and 6), the minimum number of parasite detected is 4 (Figure 11).

EQUIVALENTS

Those skilled in the art will appreciate that the invention described herein is susceptible to variations and modifications other than those specifically described. The invention also includes all of the steps, features, composition and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations of any two or more of said steps or features.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(I) APPLICANT: THE NATIONAL UNIVERSITY OF SINGAPORE

(ii) TITLE OF INVENTION: DIAGNOSIS OF PARASITES

10

(iii) NUMBER OF SEQUENCES: 22

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

25

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10 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5849 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1711 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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ACTTGAACTC AGAACCATTC GATTAAAAGT CGAGTACTCT ACCAATTAAG CTAGTAATTC 240
35 TTAATATAAC GAATCTGACG AGAATTGAAC TCGTATTCTT TGTTATGACA AAATAATATT 300
TTAACCTAAT TAACTACAA ATTCAAATAA ATATATATAG GGAAAAGGGA TTCGAACCCT 360
40 GGTATATATA ATATCTACAT AAATGTAGCA ATTTATAGCT ATAACCACTC AGCCATTCTT 420

40

TAAATATAAT AAAAAAGGAA GATTTAATT TTTAACATT TTTATTTTAG GAGTTAAAAA 1680

TTTTATCATA ATAATTTTAT ATTATAAAAT A 1711

5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 516 base pairs

(B) TYPE: nucleic acid

10

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Plasmodium berghei

15

(vii) IMMEDIATE SOURCE:

(B) CLONE: CLONE PRB

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTAATAGACA TGGACATAAA GGTGTTATTT CTTATATTAA TGATATTAAT GATATGCCTT 60

ATTTAAATAA CAAATACAA CCTGATTAT TTGTAAGTGC TATTGGTATA CCTTCTAGAA 120

25

TAAATATAGG TCAAATATTA GAGGGTATAT ATGGATTAAA TAGTTTATAT TTAAATAATA 180

GATATATAAT ATCTAATAAT TTAATACTA ATTATTATAA TAATTATATT AATAATTTTA 240

30

ATTATTATAA ATATAATTAT AATAATAATT TTGAATTCAA TAAAATATCA TATAATTATA 300

ATAAATATTT TTTAAAAAAT CCGTTTACGG GCCATTTAAT ACAGAATAGT ATTTGTTTAA 360

ATAATATTTA TTATTATAAA TTAGTACATA TGGTAAAAGA TAAATTAAGA TATAGATTCA 420

35

TAGGATTATA TTCTGAATTA ACTCACAAC CTGTAAAAGG AAATACAAA CAAGGAGGTC 480

AAAGATTGGG TGAAATGGAA GTATGGGCCG TAGAAG 516

40

(2) INFORMATION FOR SEQ ID NO:4;

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs
- (B) TYPE: nucleic acid

5

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Plasmodium berghei

10

(vii) IMMEDIATE SOURCE:

- (B) CLONE: CLONE PWQ

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTTCAAAAAT CAGATTGAC TGATAACACA TGGAACTTCA ATCCATTGCT CTACCATTGA 60
GCTATAATGA CTTAATAATA TTATTATTAT AATAGAATAT AACCAAAGG TTAAGGTAAT 120
GAACTTIGAT TTCATTAAATA TAGGTTGAA TCCTTTAGGA C 161

25

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

35

GACCTGCATG AAAGATG

17

40

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTATCGCTTT AATAGGCG

18

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCCACTACTA TGAAAATC

18

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

40 GCGTTCATTC TGAGCTAG

18

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGGTAATAC AGAAAATGCA AGCG

24

15

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGCACGAACT GACGACAGCC ATGCAC

26

30

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAGGAATA CGTCTAGG

18

(2) INFORMATION FOR SEQ ID NO:12:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15 GCTAGTATTA TGTCTTCT

18

(2) INFORMATION FOR SEQ ID NO:13:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACCATTAAAG TACATCAC

18

30

(2) INFORMATION FOR SEQ ID NO:14:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

5 TGTTAATACA ACTCCAAT

18

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCTAGTATTA TGTCTTCA

18

20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGAATGTTAT TGCTAACAC

19

(2) INFORMATION FOR SEQ ID NO:17:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

5 GTAATCAATC TATGATAC

18

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AATGAAGAGC TGTGTATC

18

20 (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

30

GCGATAAGCC GACATCGAGG TGCC

24

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

5 TATCGTGTG CATCGAATTA AGCC

24

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCTCGACTAC CATTTTAATA TCAATACCTA CCGGTA

36

20 (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

30

AGGTGCAATT ATTGCATTGT TTACATTAGT AAGTA

35

CLAIMS

1. A method of detecting a *Plasmodium* malarial agent of humans in a biological sample comprising contacting a probe or primer of the *Plasmodium berghei* extrachromosomal
5 genetic element with said sample or nucleic acid derived therefrom for a time and under conditions sufficient for hybridisation to occur and then detecting said hybridisation using a detection means, wherein the probe or primer is at least 15 nucleotides in length and comprises a nucleotide sequence that is highly conserved in *Plasmodium berghei* and said malarial agent of humans or a complementary nucleotide sequence thereto.
10
2. The method according to claim 1 wherein the extrachromosomal genetic element is the *Plasmodium berghei* plastid or plastid-like molecule.
3. The method according to claim 2 wherein the probe or primer comprises a nucleotide
15 sequence of the *Plasmodium berghei* plastid-localised LSU rRNA genes or a complementary nucleotide sequence thereto.
4. The method according to claim 3 wherein the probe or primer comprises an LSU
20 rRNA gene or gene fragment that is highly conserved between *Plasmodium berghei* isolate and the malarial agents of humans, wherein said gene or gene fragment comprises a *P. berghei* nucleotide sequence set forth in nucleotides 1147 to 1740 of SEQ ID NO:1 or any one of SEQ ID NOS: 5, 6, 19 or 20 or a complementary sequence thereto.
5. The method according to any one of claims 1 to 4 wherein the hybridisation step is
25 performed under low stringency hybridisation conditions.
6. The method according to any one of claims 1 to 4 wherein the hybridisation step is performed under moderate stringency hybridisation conditions.
- 30 7. The method according to any one of claims 1 to 4 wherein the hybridisation step is

performed under high stringency hybridisation conditions.

8. The method according to any one of claims 1 to 7 wherein the detection means used to detect the hybridisation comprises identifying a signal produced by a reporter molecule
5 bound to the probe or primer, wherein the reporter molecule is capable of producing an identifiable signal.

9. The method according to claim 8 wherein the reporter molecule is a radioisotope or a non-isotopic reporter molecule such as biotin.

10

10. The method according to any one of claims 1 to 7 wherein the detection means comprises a polymerase chain reaction (PCR) format using one or more *Plasmodium* genus-specific primers or primer pairs.

15 11. The method according to claim 10 wherein the PCR format comprises RT-PCR.

12. The method according to claim 10 or 11 wherein the genus-specific primer pairs comprise SEQ ID NOs: 5 and 6.

20 13. The method according to any one of claims 1 to 12 wherein the *Plasmodium* malarial agent of humans is selected from the list consisting of *Plasmodium falciparum*, *Plasmodium vivax*, *Plasmodium ovale* and *Plasmodium malariae*.

14. The method according to any one of claims 1 to 13 wherein the biological sample
25 comprises blood or a derivative thereof.

15. The method according to claim 14 wherein the biological sample comprises dried blood.

30 16. A method of detecting a particular species of the *Plasmodium* malarial agent of

humans in a biological sample comprising nucleic acid with a *Plasmodium* species-specific extrachromosomal genetic element probe or primer for a time and under conditions sufficient for hybridisation to occur and then detecting said hybridisation using a detection means, wherein the probe or primer is at least 15 nucleotides in length and comprises a nucleotide
5 sequence that hybridises specifically to the nucleic acid of the extrachromosomal genetic element of one species of a *Plasmodium* malarial agent of humans.

17. The method according to claim 16 wherein the probe or primer hybridises specifically to nucleic acid of the mitochondrial *coxI* gene of *Plasmodium falciparum* or *Plasmodium*
10 *vivax* or *Plasmodium ovale* or *Plasmodium malariae*.

18. The method according to claim 17 wherein the probe or primer hybridises specifically to a non-conserved or less-conserved nucleotide sequence of the mitochondrial *coxI* gene of *Plasmodium falciparum* or *Plasmodium vivax* or *Plasmodium ovale* or *Plasmodium malariae*
15 as determined from a nucleotide sequence alignment of several isolates of said species.

19. The method according to claim 18 wherein the probe comprises a nucleotide sequence that set forth in SEQ ID NOs: 21 or 22 or a complementary nucleotide sequence thereto.

20. The method according to claim 18 wherein the primer comprises a nucleotide sequence set forth in any one of SEQ ID NOs: 11-18.

21. The method according to any one of claims 16 to 20 wherein the hybridisation step is performed under low stringency hybridisation conditions.
25

22. The method according to any one of claims 16 to 20 wherein the hybridisation step is performed under moderate stringency hybridisation conditions.

23. The method according to any one of claims 16 to 20 wherein the hybridisation step
30 is performed under high stringency hybridisation conditions.

24. The method according to any one of claims 16 to 20 wherein the detection means used to detect the hybridisation comprises identifying a signal produced by a reporter molecule bound to the probe or primer, wherein the reporter molecule is capable of producing an identifiable signal.

5

25. The method according to claim 24 wherein the reporter molecule is a radioisotope or a non-isotopic reporter molecule such as biotin.

26. The method according to any one of claims 16 to 23 wherein the detection means
10 comprises a polymerase chain reaction (PCR) format using one or more *Plasmodium* species-specific primers or primer pairs.

27. The method according to claim 26 wherein the PCR format comprises RT-PCR.

15 28. The method according to claims 26 or 27 wherein the *Plasmodium* species-specific primer pairs are selected from the group consisting of: SEQ ID NOs: 11 and 12; SEQ ID NOs: 13 and 14; SEQ ID NOs: 11 and 15; SEQ ID NOs: 11 and 16; SEQ ID NOs: 11 and 17; and SEQ ID NOs: 16 and 18.

20 29. A method of detecting *Plasmodium falciparum* or or *Plasmodium vivax* or *Plasmodium ovale* or *Plasmodium malariae* in a sample comprising blood or a derivative of a blood sample such as dried blood, comprising:

(i) detecting *Plasmodium* LSU rRNA gene sequences in said sample by:

25 (a) hybridising a nucleic acid probe comprising the *P. berghei* nucleotide sequence set forth in SEQ ID NOs: 19 or 20 or a complementary nucleotide sequence to said sample or nucleic acid derived therefrom; or

(b) amplifying LSU rRNA gene sequences from said sample or nucleic acid derived therefrom in a PCR format using the primer pair comprising SEQ ID NOs: 5 and 6; and

30 (ii) detecting specific *Plasmodium falciparum* or *Plasmodium vivax* or *Plasmodium*

ovale or *Plasmodium malariae* mitochondrial *coxI* gene sequences in said sample by:

(a) hybridising a nucleic acid probe comprising the nucleotide sequence set forth in SEQ ID NOS: 21 or 22 or a complementary nucleotide sequence to said sample or nucleic acid derived therefrom; or

(b) amplifying *coxI* gene sequences from said sample or nucleic acid derived therefrom in a PCR format using one or more primer pairs selected from the group consisting of: SEQ ID NOs: 11 and 12; SEQ ID NOs: 13 and 14; SEQ ID NOs: 11 and 15; SEQ ID NOs: 11 and 16; SEQ ID NOs: 11 and 17; and SEQ ID NOs: 16 and 18.

10

30. A method of detecting *Plasmodium falciparum* in a sample comprising blood or a derivative of a blood sample such as dried blood, comprising detecting specific *Plasmodium falciparum* mitochondrial *coxI* gene sequences in said sample by amplifying *coxI* gene sequences from said sample or nucleic acid derived therefrom in a PCR format using one or more primer pairs selected from the group consisting of: SEQ ID NOs: 11 and 15; SEQ ID NOs: 11 and 16; SEQ ID NOs: 11 and 17; and SEQ ID NOs: 16 and 18.

31. A method of detecting *Plasmodium vivax* in a sample comprising blood or a derivative of a blood sample such as dried blood, comprising detecting specific *Plasmodium vivax* mitochondrial *coxI* gene sequences in said sample by amplifying *coxI* gene sequences from said sample or nucleic acid derived therefrom in a PCR format using one or more primer pairs selected from the group consisting of: SEQ ID NOs: 11 and 12; and SEQ ID NOs: 13 and 14.

32. An isolated probe or primer of the *Plasmodium berghei* plastid or plastid-like extrachromosomal genetic element for the genus-specific detection of *Plasmodium ssp.* selected from the group consisting of:

(i) a probe or primer comprising a nucleotide sequence set forth in any one of SEQ ID NOs: 1-6, 19 or 20 or a complementary nucleotide sequence thereto, wherein said probe or primer is at least 15 nucleotides in length; and

30

(ii) a probe or primer comprising a conserved sequence of at least 15 nucleotides in length obtainable from the alignment of nucleotide sequences set forth in Figure 9 or a complementary nucleotide sequence thereto.

5 33. The isolated probe or primer according to claim 32 wherein the nucleotide sequence of said probe or primer is determined by the method of:

(i) determining the nucleotide sequence of one or more regions of the *P. berghei* plastid or plastid-like extrachromosomal genetic element;

10 (ii) aligning the nucleotide sequence of various *Plasmodium* species according to the Needleman and Wunsch algorithm, wherein said other species is a malarial agent of humans; and

(iii) selecting the highly-conserved nucleotide sequences between *P. berghei* and said other species.

15 34. The isolated probe or primer according to claim 33 wherein aligning the nucleotide sequence of said one or more regions with the nucleotide sequence(s) of the corresponding region(s) of another *Plasmodium* species according to the Needleman and Wunsch algorithm comprises aligning the LSU rRNA gene sequences of *P. berghei*, *P. ovale*, *P. falciparum*, *P. vivax* and *P. malariae*.

20

35. An isolated probe or primer of a *Plasmodium coxI* gene for the species-specific detection a *Plasmodium* malarial agent of humans selected from the group consisting of:

25 (i) a probe or primer comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 11-18 or 21 or 22 or a complementary nucleotide sequence thereto, wherein said probe or primer is at least 15 nucleotides in length; and

(ii) a probe or primer comprising a non-conserved sequence of at least 15 nucleotides in length obtainable from the alignment of nucleotide sequences set forth in Figure 10 or a complementary nucleotide sequence thereto.

30 36. The isolated probe or primer according to claim 35 wherein the nucleotide sequence

of said probe or primer is determined by the method of:

- (i) determining the nucleotide sequence of the *coxI* genes of several isolates of different species of *Plasmodium* malarial agents of humans;
- (ii) aligning the nucleotide sequences of said *coxI* genes according to the Needleman and Wunsch algorithm; and
- (iii) selecting the non-conserved or less-conserved nucleotide sequences between said *coxI* genes; and
- (iv) testing the ability of the selected nucleotide sequences for their ability to specifically detect one species of a *Plasmodium* malarial agents of humans in a polymerase chain reaction or hybridisation assay.

37. The isolated probe or primer according to claim 36 wherein aligning the nucleotide sequences of said *coxI* genes according to the Needleman and Wunsch algorithm comprises aligning the *coxI* gene sequences of *P. ovale*, *P. falciparum*, *P. vivax* and *P. malariae* and wherein the selected non-conserved or less-conserved nucleotide sequence is tested for its ability to distinguish between one of said species and the remainder of said species.

38. An isolated *Plasmodium falciparum* species-specific primer pair selected from the group consisting of: SEQ ID NOs: 11 and 15; SEQ ID NOS: 11 and 16; SEQ ID NOs: 11 and 17; and SEQ ID NOs: 16 and 18.

39. An isolated *Plasmodium vivax* species-specific primer pair selected from the group consisting of: SEQ ID NOs: 11 and 12; and SEQ ID NOs: 13 and 14.

40. A kit for the detection of a *Plasmodium* malarial agent of humans in a biological sample comprising one or more of the isolated probes or primers according to any one of claims 33 to 38 or the primer pairs according to claims 39 or 40 and one or more reaction buffers suitable for use in a nucleic acid hybridisation reaction or polymerase chain reaction.

41. The kit according to claim 40 further comprising a *Plasmodium* nucleic acid molecule

positive standard.

42. A kit for the detection of a *Plasmodium* malarial agent of humans in a biological sample comprising one or more of the isolated probes or primers according to any one of
5 claims 34 to 37 or the primer pairs according to claims 38 or 39 and a *Plasmodium* nucleic acid molecule positive standard.

43. The kit according to any one of claims 40 to 42 comprising one or more isolated primer pairs, wherein both primers of a primer pair is provided in the same compartment at
10 a relative concentration suitable for the amplification of plastid DNA or plastid-like DNA or mitochondrial *coxI* sequences from a *Plasmodium* malarial agent of humans contained in a blood sample or derivative thereof.

44. The kit according to claim 43 wherein the relative concentration of primers is
15 suitable for the amplification of LSU rRNA or *coxI* sequences from a *Plasmodium* malarial agent of humans contained in a dried blood spot.

ABSTRACT

Detection of Plasmodium spp. by analysis of extrachromosomal DNA. It has been found that the molecular composition, physical arrangements, and nucleotide sequences of the extrachromosomal plastid-like element and mitochondrial element are highly conserved in different Plasmodium spp. The high degree of homology has been used to design genera-specific or species specific diagnostic assays with a low frequency of false negatives.

Plastid and Mitochondrial DNA sequences are disclosed. The use of the sequences is claimed for detection, prophylactic, and therapeutic treatment of plasmodium spp infection in human and other animals.

66030301 26069260

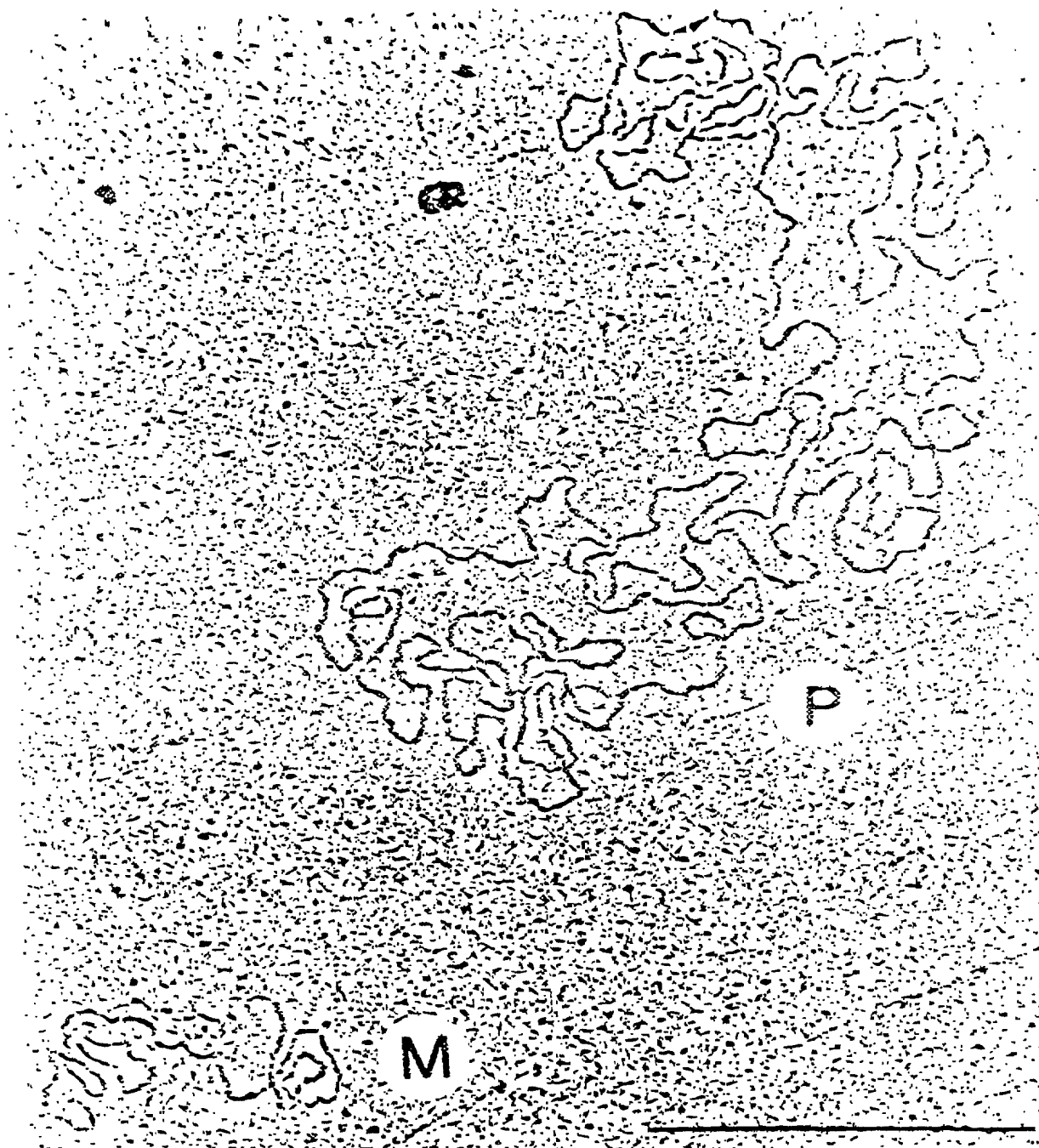


FIG. 1

A.

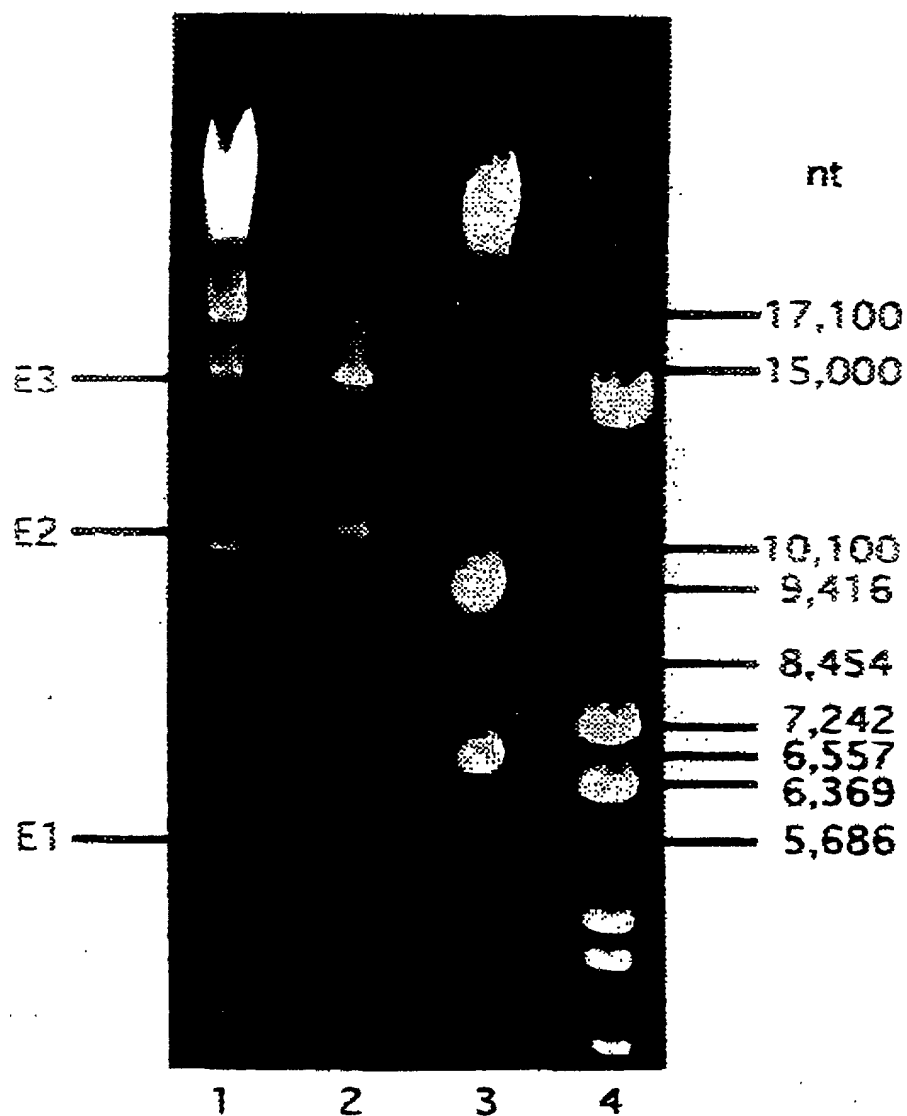


FIG. 2A

B.

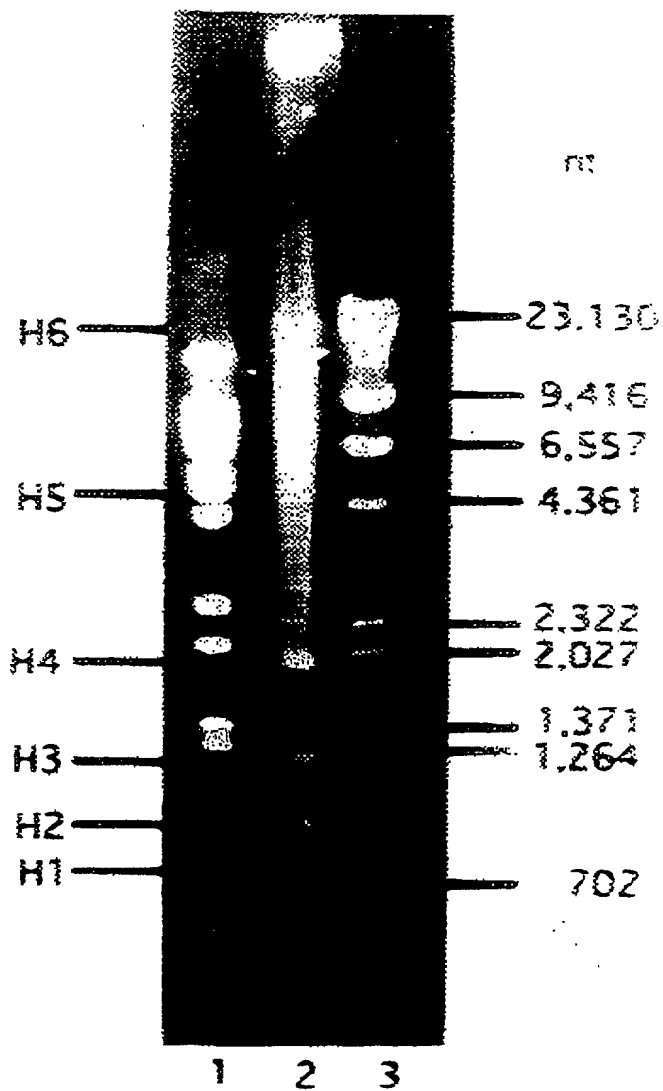


FIG. 2B

A.

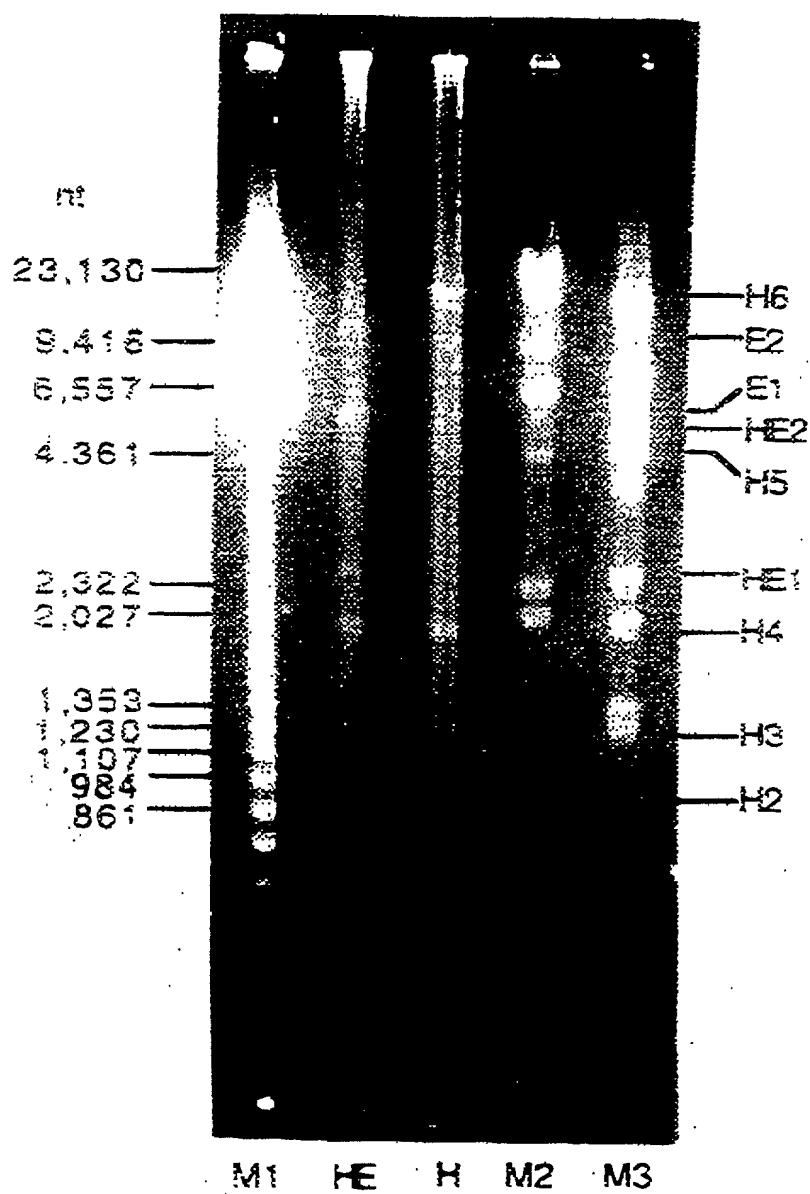


FIG. 3A

B.

C.

D.

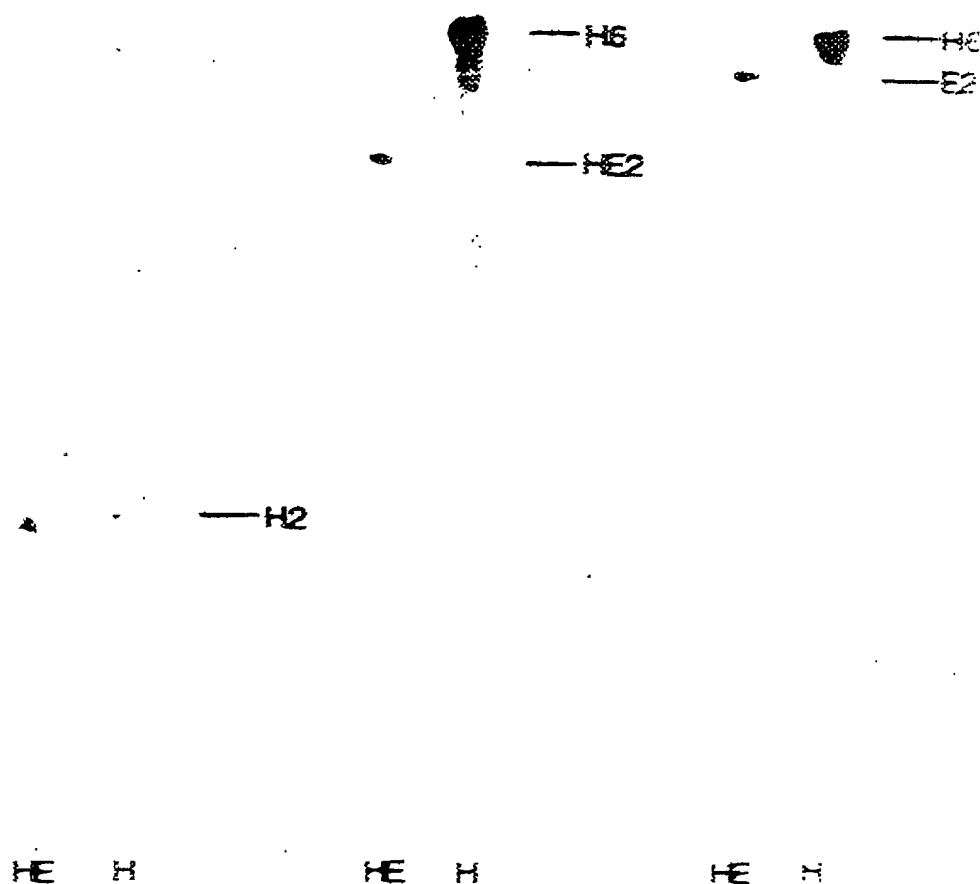


FIG. 3B

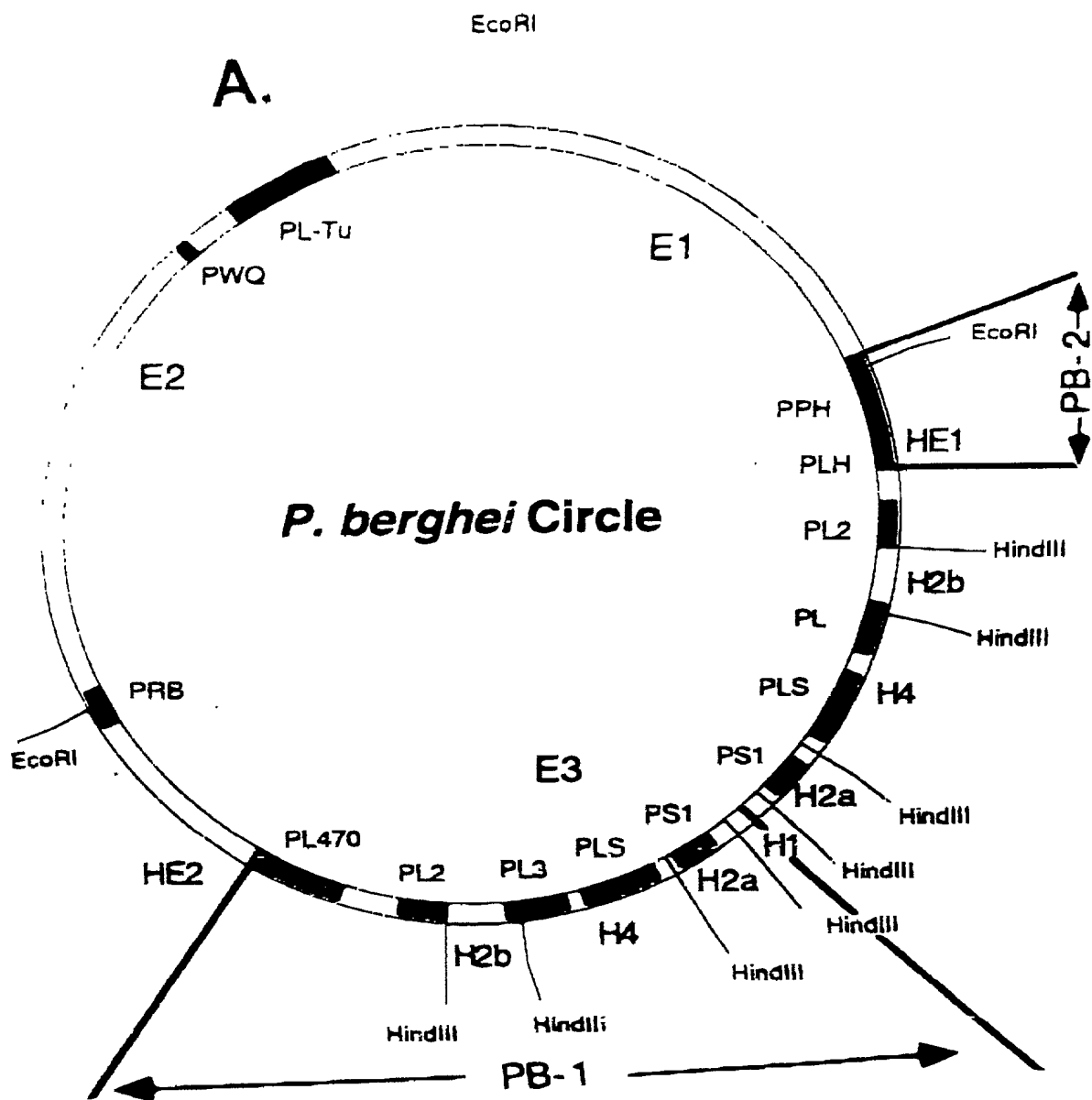


FIG. 4A

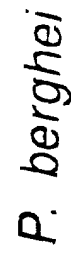


FIG. 4B

663030 6663260

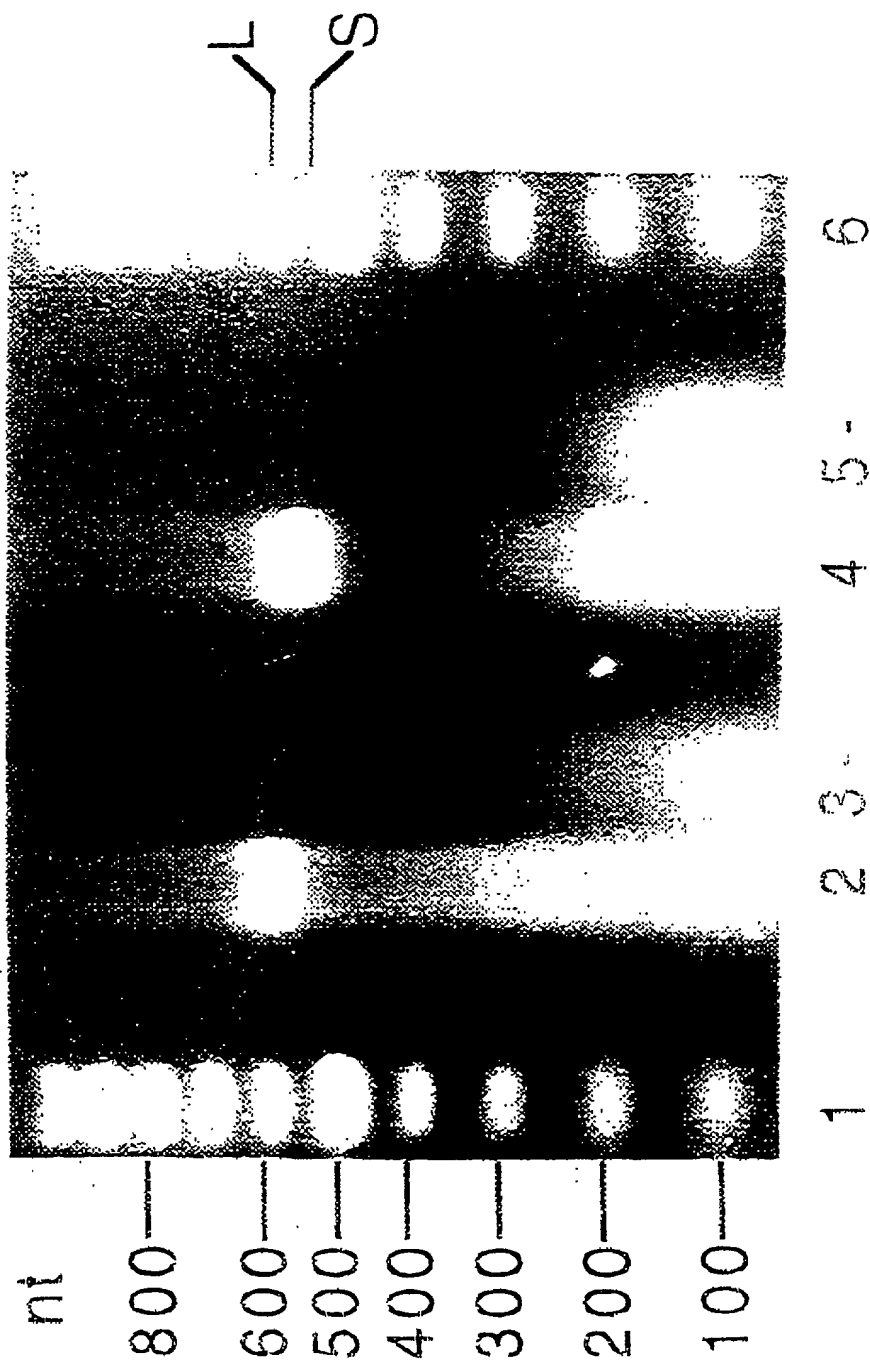


FIG. 5

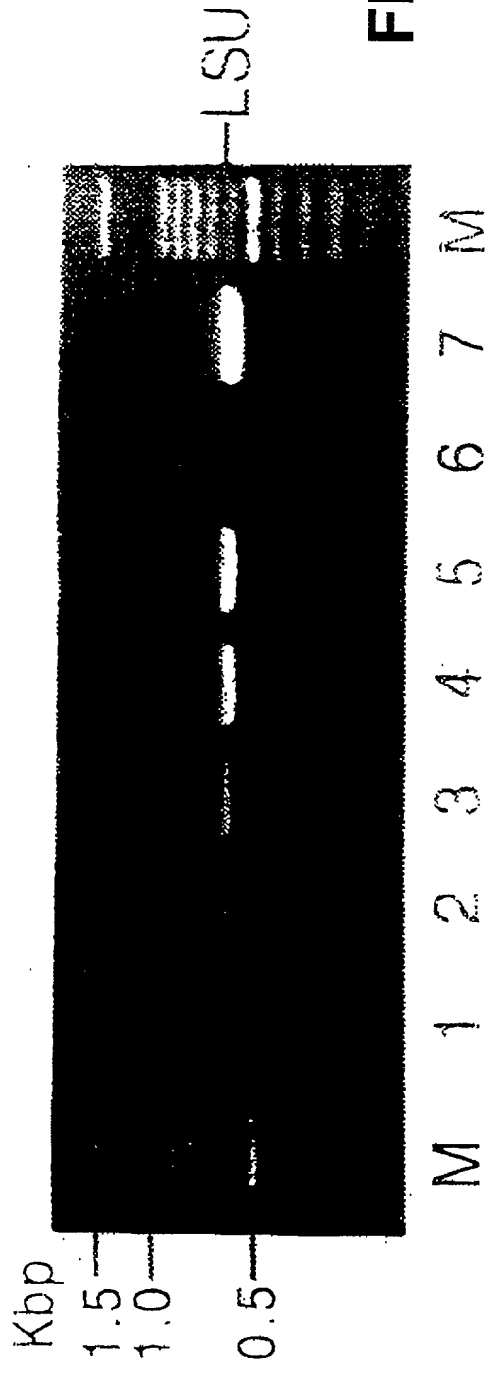


FIG. 6A

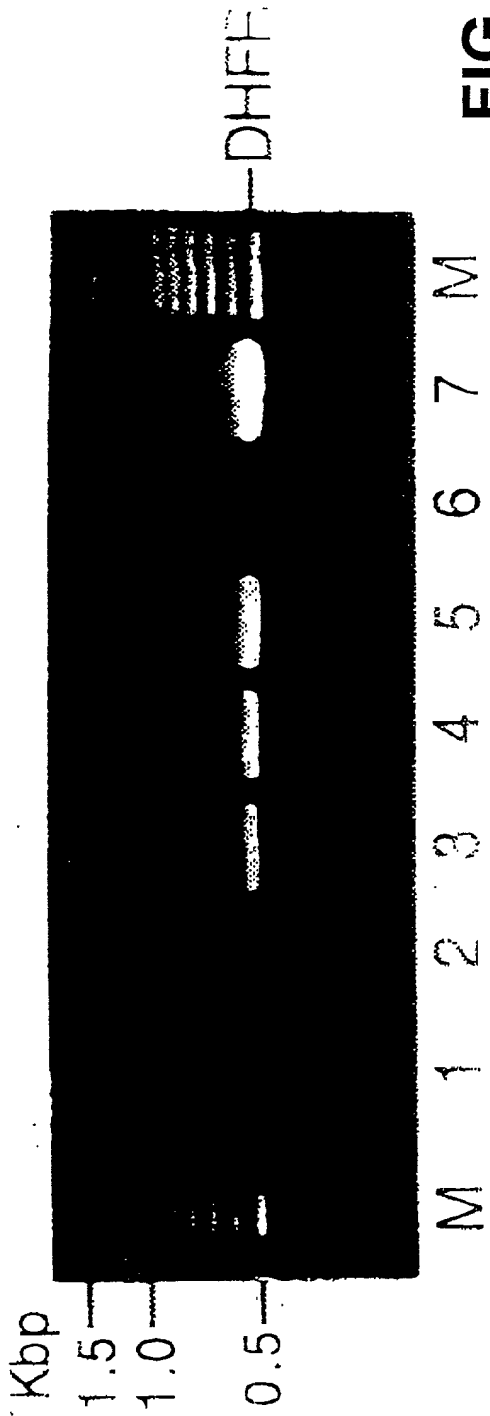


FIG. 6B

669030 256692.60

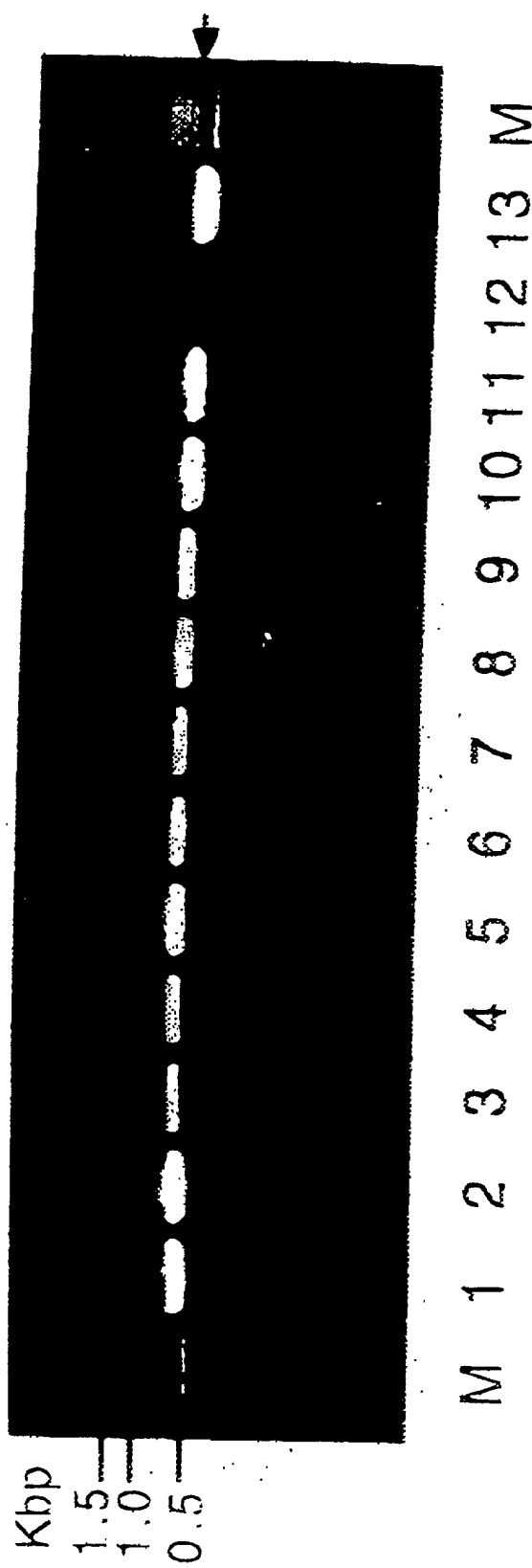


FIG. 7

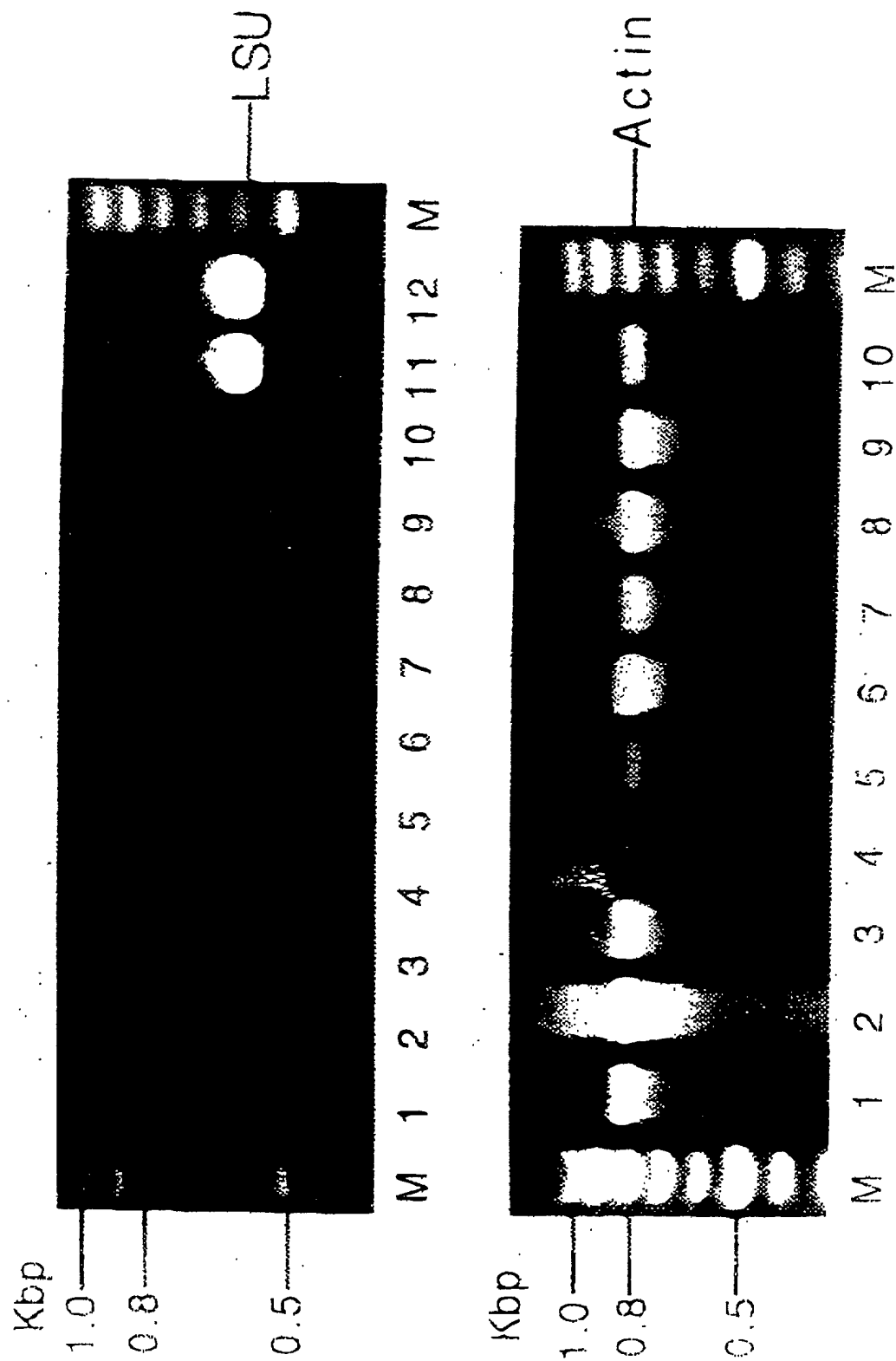


FIG. 8

FIG. 9A

61 120

Pf (C10)	AAATATCTGTGAAGATACAGATTTCTTATATTAGGACAG . AAAGACCCCTATGAAGCTTTTA
Pf10/P	AAATATCTGTGAAGATACAGATTTCTTATATTAGGACAGCAAGACCCCTATGAAGCTTTTA
Pf11/P	AAATATCTGTGAAGATACAGATGTTCTTATATTAGGACAG . AAAGACCCCTATGAAGCTTTTG
Pf19/I	AAATATCTGTGAAGATACAGATTTCTTATATTAGGACAG . AAAGACCCCTATGAAGCTTTTA
Pf20/L	AAATATCTGTGAAGATACAGATTTCTTATATTAGGACAG . AAAGACCCCTATGAAGCTTTTA
Pf18/S	AAATATCTGTGAAGATACAGATTTCTTATATTAGGACAG . GAAGACCCCTATGAAGCTTTTA
Pv12/P	AAATATCTGTGAAGATGCAGATTTCTTATATTAGGACAG . AAAGACCCCTATGAAGCTTTTA
Pv13/P	AAATATCTGTGAAGATGCAGATTTCTTATATTAGGACAG . AAAGACCCCTATGAAGCTTTTA
Pv15/I	AAATATCTGTGAAGATACAGATTTCTTATATTAGGACAG . AAAGACCCCTATGAAGCTTTTA
Pv16/L	AAATATCTGTGAAGATACAGATTTCTTATATTAGGACAG . AAAGACCCCTATGAAGCTTTTA
Pv17/S	AAATATCTGTGAAGATGCAGATTTCTTATATTAGGACAG . AAAGACCCCTATGAAGCTTTTA
Pv86/C	AAATACCTGTGAAGATGCAGATTTCTTATATTAGGACAG . AAAGACCCCTATGAAGCTTTTA
Pm1/S	AAATATCTGTGAAGATGCAGATTTCTTATATTAGGACAG . AAAGACCCCTATGAAGCTTTTA
Pm38/S	AAATATCTGTGAAGATGCAGATTTCTTATATTAGGACAG . AAAGACCCCTATGAAGCTTTTA
Po35/S	AAATATCTGTGAAGATGCAGATTTCTTATATTAGGACAG . AAAGACCCCTATGAAGCTTTTA
Po36/S	AAATATCTGTGAAGATGCAGATTTCTTATATTAGGACAG . AAAGACCCCTATGAAGCTTTTA
Pb (ANKA)	AAATATCTGTGAAGATGCAGATTTCTTATATTAGGACAG . AAAGACCCCTATGAAGCTTTTA

FIG. 9B

	121	180
Pf (C10)	CTATTAAATAAATAATGAAAAATATATATATATTAAACATAGTATAAATGGGAAACAATAATAT	
Pf10/P	CTATTAAATAAATAATGAAAAATATATATATATTAAACATAGTATAAATGGGAAACAATAATAT	
Pf11/P	CTATTAAATAAATAATGAAAAATATATATATATTAAACATAGTATAAATGGGAAACAATAATAT	
Pf19/I	CTATTAAATAAATAATGAAAAATATATATATATTAAACATAGTATAAATGGGAAACAATAATAT	
Pf20/L	CTATTAAATAAATAATGAAAAATATATATATATTAAACATAGTATAAATGGGAAACAATAATAT	
Pf18/S	CTATTAAATAAATAATGAAAAATATATATATATTAAACATAGTATAAATGGGAAACAATAATAT	
Pv12/P	CTATGAATAGATATTGAAAAATATATATATATAGAGCATAGCATAAATGGGAAATAATGATAT	
Pv13/P	CTATGAATAGATATTGAAAAATATATATATATAGAGCATAGCATAAATGGGAAATAATGATAT	
Pv15/I	CTATTAAATAAATAATGAAAAATATATATATATTAAACATAGTATAAATGGGAAACAATAATAT	
Pv16/L	CTATTAAATAAATAATGAAAAATATATATATATTAAACATAGTATAAATGGGAAACAATAATAT	
Pv17/S	CTATGAATAGATATTGAAAAATATATATATATAGAGCATAGCATAAATGGGAAATAATGATAT	
Pv86/C	CTATGAATAGATATTGAAAAATATATATATATAGAGCATAGCATAAATGGGAAATAATGATAT	
Pm1/S	CTATGAATAGATATTGAAAAATATATATATATAGAGCATAGCATAAATGGGAAATAATGATAT	
Pm38/S	CTATGAATAGATATTGAAAAATATATATATATAGAGCATAGCATAAATGGGAAATAATGATAT	
Po35/S	CTATGAATAGATATTGAAAAATATATATATATAGAGCATAGCATAAATGGGAAATAATGATAT	
Po36/S	CTATGAATAGATATTGAAAAATATATATATATAGAGCATAGCATAAATGGGAAATAATGATAT	
Pb (ANKA)	CTATTAAATAGATATTGAAAAATATATATATATAACATAGAATAAATGGGAAGTAGTAATAT	

FIG. 9C

FIG. 9D

	241		300
Pf (C10)		TATAGAAATTTATAACA.AAATTTTAAACAA.TATTTATGAGATAGTTTGACTGGGG.C	
Pf10/P		TATAGAAATTTATAACAGAAATTTTAGACAACTATTCATGAGATAGTTTGACTGGGG.C	
Pf11/P		TATAGAAATTTATAACA.AAATTTTAAACAA.TATTTATGAGATAGTTTGACTGGGG.C	
Pf19/I		TATAGAAATTTATAACA.AAATTTTAAACAA.TATTTATGAGATAGTTTGACTGGGG.C	
Pf20/L		TATAGAAATTTATAACA.AAATTTTAAACAA.TATTTATGAGATAGTTTGACTGGGG.C	
Pf18/S		TATAGAAATTTATAACA.AAATTTTAAACAA.TATTTATGAGATAGTTTGACTGGGG.C	
Pv12/P		TAAAAAAATTTTAAACA.AAATTTTAAACAG.TATTTATAAGATAGTTTGACTGGGG.C	
Pv13/P		TAAAAAAATTTTAAACA.AAATTTTAAACAG.TATTTATAAGATAGTTTGACTGGGG.C	
Pv15/I		TATAGAAATTTATAACA.AAATTTTAAACAA.TATTTATGAGATAGTTTGACTGGGG.C	
Pv16/L		TATAGAAATTTATAACA.AAATTTTAAACAA.TATTTATGAGATAGTTTGACTGGGG.C	
Pv17/S		TAAAAAAATTTTAAACA.AAATTTTAAACAG.TATTTATAAGATAGTTTGACTGGGG.C	
Pv86/C		TAAAAAAATTTTAAACA.AAATTTTAAACAG.TATTTATAAGATAGTTTGACTGGGG.C	
Pm1/S		TAAAAAAATTTT.AACA.AAATTTTAAACAG.TATTTATAAGATAGTTTGACTGGGG.C	
Pm38/S		TAAAAAAATTTTAAACA.AAATTTTAAACAG.TATTTATAAGATAGTTTGACTGGGGC	
Po35/S		TAAAAAAATTTTAAACA.AAATTTTAAACAG.TATTTATAAGATAGTTTGACTGGGG.C	
Po36/S		TAAAAAAATTTTAAACA.AAATTTTAAACAG.TATTTATAAGATAGTTTGACTGGGG.C	
Pb (ANKA)		TATAAAATTTTATAACA.AAATTTTAAACAA.TATTTATAAGATAGTTTGACTGGGG.C	

FIG. 9E

	301	GGTCTCCTCCTATATAA	360	GGTCTCCTCCTATATAA
Pf (C10)		GGTCTCCTCCTATATAA		GGTCTCCTCCTATATAA
Pf10/P		GGTCTCCTCCTATATAA		GGTCTCCTCCTATATAA
Pf11/P		GGTCTCCTCCTATATAA		GGTCTCCTCCTATATAA
Pf19/I		GGTCTCCTCCTATATAA		GGTCTCCTCCTATATAA
Pf20/L		GGTCTCCTCCTATATAA		GGTCTCCTCCTATATAA
Pf18/S		GGTCTCCTCCTATATAA		GGTCTCCTCCTATATAA
Pv12/P		GGTCTCCTCCTATATAA		GGTCTCCTCCTATATAA
Pv13/P		GGTCTCCTCCTATATAA		GGTCTCCTCCTATATAA
Pv15/I		GGTCTCCTCCTATATAA		GGTCTCCTCCTATATAA
Pv16/L		GGTCTCCTCCTATATAA		GGTCTCCTCCTATATAA
Pv17/S		GGTCTCCTCCTATATAA		GGTCTCCTCCTATATAA
Pv86/C		GGTCTCCTCCTATATAA		GGTCTCCTCCTATATAA
Pm1/S		GGTCTCCTCCTATATAA		GGTCTCCTCCTATATAA
Pm38/S		GGTCTCCTCCTATATAA		GGTCTCCTCCTATATAA
Po35/S		GGTCTCCTCCTATATAA		GGTCTCCTCCTATATAA
Po36/S		GGTCTCCTCCTATATAA		GGTCTCCTCCTATATAA
Pb (ANKA)		GGTCTCCTCCTATATAA		GGTCTCCTCCTATATAA

FIG. 9F

	361		420
Pf (C10)		TATATAATTAACTGTAAAAATTTACAAAATTAAACAGAGATAAAATGTCGGTCTTAAATGATCC	
Pf10/P		TATATAATTAACTGTAAAAATTTACAAAATTAAACAGAGATAAAATGTCGGTCTTAAATGATCC	
Pf11/P		TATATAATTAACTGTAAAAATTTACAAAATTAAACAGAGATAAAATGTCGGTCTTAAATGATCC	
Pf19/I		TATATAATTAACTGTAAAAATTTACAAAATTAAACAGAGATAAAATGTCGGTCTTAAATGATCC	
Pf20/L		TATATAATTAACTGTAAAAATTTACAAAATTAAACAGAGATAAAATGTCGGTCTTAAATGATCC	
Pf18/S		TATATAATTAACTGTAAAAATTTACAAAATTAAACAGAGATAAAATGTCGGTCTTAAATGATCC	
Pv12/P		TATATAATTAACTGTAAAAATTTACAAAATTAAACAGAGATTAATGTCGGTCTTAAATGATCC	
Pv13/P		TATATAATTAACTGTAAAAATTTACAAAATTACACAGAGATTAATGTCGGTCTTAAATGATCC	
Pv15/I		TATATAATTAACTGTAAAAATTTACAAAATTAAACAGAGATAAAATGTCGGTCTTAAATGATCC	
Pv16/L		TATATAATTAACTGTAAAAATTTACAAAATTAAACAGAGATAAAATGTCGGTCTTAAATGATCC	
Pv17/S		TATATAATTAACTGTAAAAATTTACAAAATTAAACAGAGATTAATGTCGGTCTTAAATGATCC	
Pv86/C		TATATAATTAACTGTAAAAATTTGACAAAATTAAACAGAGATTAATGTCGGTCTTAAATGATCC	
Pm1/S		TATATAATTAACTGTAAAAATTTAACAAAATTAAACAGAGATTAATGTCGGTCTTAAATGATCC	
Pm38/S		TATATAATTAACTGTAAAAATTTAACAAAGTTAAACAGAGATTAATGTCGGTCTTAAATGATCC	
Po35/S		TATATAATTAACTGTAAAAATTTACAAAATTAAACAGAGATTAATGTCGGTCTTAAATGATCC	
Po36/S		TATATAATTAACTGTAAAAATTTACAAAATTAAACAGAGATTAATGTCGGTCTTAAATGATCC	
Pb (ANKA)		TATATAATTAACTGTAAAAATTTACAAAATTAAACAGAGATTAATGTCGGTCTTAAATGATCC	

FIG. 9G

Pf (C10)	421	GATAATTATTTAGTAATAAAATATATCGCTTAACGGATAAAAAGTTACTCTAGGGATAACAG	480
Pf10/P		GATAATTATTTAGTAATAAAATATATCGCTTAACGGATAAAAAGTTACTCTAGGGATAACAG	
Pf11/P		GATAATTATTTAGTAATAAAATATATCGCTTAACGGATAAAAAGTTACTCTAGGGATAACAG	
Pf19/I		GATAATTATTTAGTAATAAAATATATCGCTTAACGGATAAAAAGTTACTCTAGGGATAACAG	
Pf20/L		GATAATTATTTAGTAATAAAATATATCGCTTAACGGATAAAAAGTTACTCTAGGGATAACAG	
Pf18/S		GATAATTATTTAGTAATAAAATATATCGCTTAACGGATAAAAAGTTACTCTAGGGATAACAG	
Pv12/P		GATAATTATTTAGTAATAAAATATATCGCTTAACGGATAAAAAGTTACTCTAGGGATAACAG	
Pv13/P		GATAATTATTTAGTAATAAAATATATCGCTTAACGGATAAAAAGTTACTCTAGGGATAACAG	
Pv15/I		GATAATTATTTAGTAATAAAATATATCGCTTAACGGATAAAAAGTTACTCTAGGGATAACAG	
Pv16/L		GATAATTATTTAGTAATAAAATATATCGCTTAACGGATAAAAAGTTACTCTAGGGATAACAG	
Pv17/S		GATAATTATTTAGTAATAAAATATATCGCTTAACGGATAAAAAGTTACTCTAGGGATAACAG	
Pv86/C		GATAATTATTTAGTAATAAAATATATCGCTTAACGGATAAAAAGTTACTCTAGGGATAACAG	
Pm1/S		GATAATTATTTAGTAATAAAATATATCGCTTAACGGATAAAAAGTTACTCTAGGGATAACAG	
Pm38/S		GATAATTATTTAGTAATAAAATATATCGCTTAACGGATAAAAAGTTACTCTAGGGATAACAG	
Po35/S		GATAATTATTTAGTAATAAAATATATCGCTTAACGGATAAAAAGTTACTCTAGGGATAACAG	
Po36/S		GATAATTATTTAGTAATAAAATATATCGCTTAACGGATAAAAAGTTACTCTAGGGATAACAG	
Pb (ANKA)		GATAATTATTTAGTAATAAAATATATCGCTTAACGGATAAAAAGTTACTCTAGGGATAACAG	

FIG. 9H

Pf (C10)	481	GCTAAATCTTTTCCGAGAGTCCATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTAT	540
Pf10/P		GCTAAATCTTTTCCGAGAGTCCATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTAT	
Pf11/P		GCTAAATCTTTTCCGAGAGTCCATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTAT	
Pf19/I		GCTAAATCTTTTCCGAGAGTCCATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTAT	
Pf20/L		GCTAAATCTTTTCCGAGAGTCCATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTAT	
Pf18/S		GCTAAATCTTTTCCGAGAGTCCATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTAT	
Pv12/P		GCTAAATCTTTTCCGAGAGTCCATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTAT	
Pv13/P		GCTAAATCTTTTCCGAGAGTCCATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTAT	
Pv15/I		GCTAAATCTTTTCCGAGAGTCCATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTAT	
Pv16/L		GCTAAATCTTTTCCGAGAGTCCATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTAT	
Pv17/S		GCTAAATCTTTTCCGAGAGTCCATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTAT	
Pv86/C		GCTAAATCTTTTCCGAGAGTCCATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTAT	
Pm1/S		GCTAAATCTTTTCCGAGAGTCCATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTAT	
Pm38/S		GCTAAATCTTTTCCGAGAGTCCATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTAT	
Po35/S		GCTAAATCTTTTCCGAGAGTCCATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTAT	
Po36/S		GCTAAATCTTTTCCGAGAGTCCATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTAT	
Pb (ANKA)		GCTAAATCTTTTCCGAGAGTCCATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTAT	

FIG. 9I

541

600

Pf (C10)

CGCATCCCTAAAGCAGTAGTATGTTTAAAGGGTAAGTCTGTT

Pf10/P

CGCATCCCTAAAGCAGTAGTATGTTTAAAGGGTAAGTCTGTT

Pf11/P

CGCATCCCTAAAGCAGTAGTATGCCCCAAGGGTAAGTCTGTT

Pf19/I

CGCATCCCTAAAGCAGTAGTATGTTTAAAGGGTAAGTCTGTT

Pf20/L

CGCATCCCTAAAGCAGTAGTATGTTTAAAGGGTAAGTCTGTT

Pf18/S

CGCATCCCTAAAGCAGTAGTATGTTTAAAGGGTAAGTCTGTT

Pv12/P

CGCATCCCTAAAGCAGTAGTATGTTTAAAGGGTAAGTCTGTT

Pv13/P

CGCATCCCTAAAGCAGTAGTATGTTTAAAGGGTAAGTCTGTT

Pv15/I

CGCATCCCTAAAGCAGTAGTATGTTTAAAGGGTAAGTCTGTT

Pv16/L

CGCATCCCTAAAGCAGTAGTATGTTTAAAGGGTAAGTCTGTT

Pv17/S

CGCATCCCTAAAGCAGTAGTATGTTTAAAGGGTAAGTCTGTT

Pv86/C

CGCATCCCTAAAGCAGTAGTATGTTTAAAGGGTAAGTCTGTT

Pm1/S

CGCATCCCTAAAGCAGTAGTATGTTTAAAGGGTAAGTCTGTT

Pm38/S

CGCATCCCTAAAGCAGTAGTATGTTTAAAGGGTAAGTCTGTT

Po35/S

CGCATCCCTAAAGCAGTAGTATGTTTAAAGGGTAAGTCTGTT

Po36/S

CGCATCCCTAAAGCAGTAGTATGTTTAAAGGGTAAGTCTGTT

Pb (ANKA)

CGCATCCCTAAAGCAGTAGTATGTTTAAAGGGTAAGTCTGTT

FIG. 9J

	1		60
PfcoxI	GACTGTATGGATCAAATATTTCTCATTATATCCGAGCCTCA.....TGTTA.....		
Pf47coxI	GACTGTATGGATCGAATATTTCTCATTATATCCGAGCCTCA.....TGTTA.....		
Pv15coxI	GACTGTATGGATCGAATCTTACTTATTCATATCCAAAGCCTCAGTTATTTGTTAAATTATATA		
Pv16coxI	GACTGTATGGATCGAATCTTACTTATTCATATCCAAAGCCTCAGTTATTTGTTAAATTATATA		
Pv32coxI	GACTGTATGGATCGAATCTTACTTATTCATATCCAAAGCCTCAGTTATTTGTTAAATTATATA		
Pv37coxI	GACTGTATGGATCGAATCTTACTTATTCATATCCAAAGCCTCAGTTATTTGTTAAATTATATA		
Po35coxI	GACTGTATGGATCGAATCTTACTTATTCATATCCAAAGCCTCAGTTATTTGTTAAATTATATA		
Pm58coxI	GACTGTATGGATCGAATCTTACTTATTCATATCCAAAGCCTCAGTTATTTGTTAAATTATATA		

	61		120
PfcoxITTTTTATTTGTTTAAATAGATATTCAGTTATTAACAAATTTGTAACCATATAAACT		
Pf47coxITTTTTATTTGTTTAAATAGATATTCAGTTATTAACAAATTTGTAACCATATAAACT		
Pv15coxI	TTATATTTTTTTTTTTGTTTCCAAATAGATATACAGTTATTAACAAATTTGCAATCATATAAACT		
Pv16coxI	TTATATTTTTTTTTT..TGTTTTCAAATAGATATACAGTTATTAACAAATTTGCAATCATATAAACT		
Pv32coxI	TTATATTTTTTTTTT..TGTTTTCAAATAGATATACAGTTATTAACAAATTTGCAATCATATAAACT		
Pv37coxI	TTATATTTTTTTTTT..TGTTTTCAAATAGATATACAGTTATTAACAAATTTGCAATCATATAAACT		
Po35coxI	TTATATTTTTTTTTT..TGTTTTCAAATAGATATACAGTTATTAACAAATTTGCAATCATATAAACT		
Pm58coxI	TTATATTTTTTTTTT..TGTTTTCAAATAGATATACAGTTATTAACAAATTTGCAATCATATAAACT		

FIG. 10A

PfcoxI	121	TTAGGATTATACTATTATGGGTTTTCATTTTTCATTTTGGTAGTTATGGATTTTATTATCA	180
Pf47coxI		TTAGGATTATACTATTATGGGTTTTCATTTTTCATTTTGGTAGTTATGGATTTTATTATCA	
Pv15coxI		TTAGGTCATATACTATTATGGGTTTTCATTTTTCATTTTGGTAGTTATGGTTTATTATCT	
Pv16coxI		TTAGGTCATATACTATTATGGGTTTTCATTTTTCATTTTGGTAGTTATGGTTTATTATCT	
Pv32coxI		TTAGGTCATATACTATTATGGGTTTTCATTTTTCATTTTGGTAGTTATGGTTTATTATCT	
Pv37coxI		TTAGGTCATATACTATTATGGGTTTTCATTTTTCATTTTGGTAGTTATGGTTTATTATCT	
Po35coxI		TTAGGTCATATACTATTATGGGTTTTCATTTTTCATTTTGGTAGTTATGGTTTATTATCT	
Pm58coxI		TTAGGTCATATACTATTATGGGTTTTCATTTTTCATTTTGGTAGTTATGGTTTATTATCT	
PfcoxI	181	GTAAATACTACGTACTGAATTATATTCCTTCATCTTTAAGAAATAATTGCACAGAAAAATGTA	240
Pf47coxI		GTAAATACTACGTACTGAATTATATTCCTTCATCTTTAAGAAATAATTGCACAGAAAAATGTA	
Pv15coxI		GTATATTTACGTACAGAAATTAATTCCTTCCTTTAAGAAATAATTGCACAGAAAAATGTT	
Pv16coxI		GTATATTTACGTACAGAAATTAATTCCTTCCTTTAAGAAATAATTGCACAGAAAAATGTT	
Pv32coxI		GTATATTTACGTACAGAAATTAATTCCTTCCTTTAAGAAATAATTGCACAGAAAAATGTT	
Pv37coxI		GTATATTTACGTACAGAAATTAATTCCTTCCTTTAAGAAATAATTGCACAGAAAAATGTT	
Po35coxI		GTATATTTACGTACAGAAATTAATTCCTTCCTTTAAGAAATAATTGCACAGAAAAATGTT	
Pm58coxI		GTATATTTACGTACAGAAATTAATTCCTTCCTTTAAGAAATAATTGCACAGAAAAATGCT	

FIG. 10B

	241		300
PfcoxI		AACTATATAATGATATTACAAATTCACGGAATAATTATGATTTTTTCAATATAATG	
Pf47coxI		AACTATATAATGATATTACAAATTCACGGAATAATTATGATTTTTTCAATATAATG	
Pv15coxI		AACTTATATAATGATATTACATTACATGGAATTTATGATATTTCTTAATATAATG	
Pv16coxI		AACTTATATAATGATATTACATTACATGGAATTTATGATATTTCTTAATATAATG	
Pv32coxI		AACTTATATAATGATATTACATTACATGGAATTTATGATATTTCTTAATATAATG	
Pv37coxI		AACTTATATAATGATATTACATTACATGGAATTTATGATATTTCTTAATATAATG	
Po35coxI		AACTTATATAATGATATTACATTACATGGAATTTATGATATTTCTTAATATAATG	
Pm58coxI		AACTTATATAATGATATTACATTACATGGAATTTATGATATTTCTTAATATAATG	
	301		360
PfcoxI		CCAGGATTTATTCGGAGGATTTGGTAATTACTTTCTACCTATTTTATGTGGATCTCCAGAA	
Pf47coxI		CCAGGATTTATTCGGAGGATTTGGTAATTACTTTCTACCTATTTTATGTGGATCTCCAGAA	
Pv15coxI		CCAGGATTTATTCGGAGGATTCGGTAATTACTTCTACCAATTTTATGTGGTTCTCCAGAA	
Pv16coxI		CCAGGATTTATTCGGAGGATTCGGTAATTACTTCTACCAATTTTATGTGGTTCTCCAGAA	
Pv32coxI		CCAGGATTTATTCGGAGGATTCGGTAATTACTTCTACCAATTTTATGTGGTTCTCCAGAA	
Pv37coxI		CCAGGATTTATTCGGAGGATTCGGTAATTACTTCTACCAATTTTATGTGGTTCTCCAGAA	
Po35coxI		CCAGGATTTATTCGGAGGATTCGGTAATTACTTCTACCAATTTTATGTGGTTCTCCAGAA	
Pm58coxI		CCAGGATTTATTCGGAGGATTCGGTAATTACTTCTACCAATTTTATGTGGTTCTCCAGAA	

FIG. 10C

	361		420
PfcoxI	TTAGCATATCCTAGAA	TTAATAGTATATCTTTACTGTTACAACCAATTGCTTTTGTTTTA	
Pf47coxI	TTAGCATATCCTAGAA	TTAATAGTATATCTTTACTGTTACAACCAATTGCTTTTGTTTTA	
Pv15coxI	CTTGCAATATCCAAGA	ATTAATAGTATATCTTTATTTATTAACAACCAATAGCTTTTATATATTA	
Pv16coxI	CTTGCAATATCCAAGA	ATTAATAGTATATCTTTATTTATTAACAACCAATAGCTTTTATATATTA	
Pv32coxI	CTTGCAATATCCAAGA	ATTAATAGTATATCTTTATTTATTAACAACCAATAGCTTTTATATATTA	
Pv37coxI	CTTGCAATATCCAAGA	ATTAATAGTATATCTTTATTTATTAACAACCAATAGCTTTTATATATTA	
Po35coxI	CTTGCAATATCCAAGA	ATTAATAGTATATCTTTATTTATTAACAACCAATAGCTTTTATATATTA	
Pm58coxI	CTTGCAATATCCAAGA	ATTAATAGTATATCTTTATTTATTAACAACCAATAGCTTTTATATATTA	
	421		480
PfcoxI	GTATATATTACTGCAGCAGAA	TTGGTGGTGGAACTGGATGGACTTTTATATCCACCA	
Pf47coxI	GTATATATTACTGCAGCAGAA	TTGGTGGTGGAACTGGATGGACTTTTATATCCACCA	
Pv15coxI	GTCAATTTTATCTACAGCAGCAGAA	TTGGAGGAGGTACTGGATGGACTTTTATATCCACCA	
Pv16coxI	GTAAATTTTATCTACAGCAGCAGAA	TTGGAGGAGGTACTGGATGGACTTTTATATCCACCA	
Pv32coxI	GTCAATTTTATCTACA	CTCAGGAGGTACTGGATGGACTTTTATATCCACCA	
Pv37coxI	GTCAATTTTATCTACAGCAGCAGAA	TTGGAGGAGGTACTGGATGGACTTTTATATCCACCA	
Po35coxI	GTCAATTTTATCTACAGCAGCAGAA	TTGGAGGAGGTACTGGATGGACTTTTATATCCACCA	
Pm58coxI	GTCAATTTTATCTACAGCAGCAGAA	TTGGAGGAGGTACTGGATGGACTTTTATATCCACCA	

FIG. 10D

	481		540
Pfcox1	TTAAGTACATCTTTAAATGTCATTAATCTCCCTGTAGCTGTAGATGTAATAATTTTGGTTTA		
Pf47cox1	TTAAGTACATCTTTAAATGTCATTAATCTCCCTGTAGCTGTAGATGTAATAATTTTGGTTTA		
Pv15cox1	TTAAGTACATCACTTATGTCTTTATCTCCCTGTGCAGTAGATGTTATCATTTGTTGGTCTT		
Pv16cox1	TTAAGTACATCACTTATGTCTTTATCTCCCTGTGCAGTAGATGTTATCATTTGTTGGTCTT		
Pv32cox1	TTAAGTACATCACTTATGTCTTTATCTCCCTGTGCAGTAGATGTTATCATTTGTTGGTCTT		
Pv37cox1	TTAAGTACATCACTTATGTCTTTATCTCCCTGTGCAGTAGATGTTATCATTTGTTGGTCTT		
Po35cox1	TTAAGTACATCACTTATGTCTTTATCTCCCTGTGCAGTAGATGTTATCATTTGTTGGTCTT		
Pm58cox1	TTAAGTACATCACTTATGTCTTTATCTCCCTGTGCAGTAGATGTTATCATTTGTTGGTCTT		
	541		600
Pfcox1	TTAGTATCTGGAGTCGCTAGTATTATGTCTTCATTAAATTTTATTACTACAGTAATGCAT		
Pf47cox1	TTAGTATCTGGAGTCGCTAGTATTATGTCTTCATTAAATTTTATTACTACAGTAATGCAT		
Pv15cox1	TTAGTATCTGGTATTGCTAGTATTATGTCTCTTTAAATTTTATTACTACTGTAATGCAT		
Pv16cox1	TTAGTATCTGGTATTGCTAGTATTATGTCTCTTTAAATTTTATTACTACTGTAATGCAT		
Pv32cox1	TTAGTATCTGGTATTGCTAGTATTATGTCTCTTTAAATTTTATTACTACTGTAATGCAT		
Pv37cox1	TTAGTATCTGGTATTGCTAGTATTATGTCTCTTTAAATTTTATTACTACTGTAATGCAT		
Po35cox1	TTAGTATCTGGTATTGCTAGTATTATGTCTCTTTAAATTTTATTACTACTGTAATGCAT		
Pm58cox1	TTAGTATCTGGTATTGCTAGTATTATGTCTCTTTAAATTTTATTACTACTGTAATGCAT		

FIG. 10E

PfcoxI	660	TTAAGAGCAAAAGGATTAAACACTTGGTATATTAAAGTGTTCCTACATGGTCATTGATCATTT
Pf47coxI		TTAAGAGCAAAAGGATTAAACACTTGGTATATTAAAGTGTTCCTACATGGTCATTGATCATTT
Pv15coxI		CTAAGATCTAAAGGTTTAAACACTTGGTATATTAAAGTGTATCTACATGGTCATTAAATAATT
Pv16coxI		CTAAGATCTAAAGGTTTAAACACTTGGTATATTAAAGTGTATCTACATGGTCATTAAATAATT
Pv32coxI		CTAAGATCTAAAGGTTTAAACACTTGGTATATTAAAGTGTATCTACATGGTCATTAAATAATT
Pv37coxI		CTAAGATCTAAAGGTTTAAACACTTGGTATATTAAAGTGTATCTACATGGTCATTAAATAATT
Po35coxI		CTAAGATCTAAAGGTTTAAACACTTGGTATATTAAAGTGTATCTACATGGTCATTAAATAATT
Pm58coxI		CTAAGATCTAAAGGTTTAAACACTTGGTATATTAAAGTGTATCTACATGGTCATTAAATAATT
PfcoxI	720	ACATCAGGAAATGTTATTGCTAAACACTACCGGTTTTTAACTGGAGGAGTATTAAATGTTATTAA
Pf47coxI		ACATCAGGAAATGTTATTGCTAAACACTACCGGTTTTTAACTGGAGGAGTATTAAATGTTATTAA
Pv15coxI		ACATCTGTAAATGCTATTATTAAACATTACCTGTCTTTTAAACAGGTGGTGTCTTTTAAATGTTATTAA
Pv16coxI		ACATCTGTAAATGCTATTATTAAACATTACCTGTCTTTTAAACAGGTGGTGTCTTTTAAATGTTATTAA
Pv32coxI		ACATCTGTAAATGCTATTATTAAACATTACCTGTCTTTTAAACAGGTGGTGTCTTTTAAATGTTATTAA
Pv37coxI		ACATCTGTAAATGCTATTATTAAACATTACCTGTCTTTTAAACAGGTGGTGTCTTTTAAATGTTATTAA
Po35coxI		ACATCTGTAAATGCTATTATTAAACATTACCTGTCTTTTAAACAGGTGGTGTCTTTTAAATGTTATTAA
Pm58coxI		ACATCTGTAAATGCTATTATTAAACATTACCTGTCTTTTAAACAGGTGGTGTCTTTTAAATGTTATTAA

FIG. 10F

721 780
 pfcoxI TCAGACTTACATTTTAATACTTTTATTTTGGACCCCAACATTTGCAGGAGATCCAATATTA
 pf47coxI TCAGACTTACATTTTAATACTTTTATTTTGGACCCCAACATTTGCAGGAGATCCAATATTA
 pv15coxI TCAGATTTACATTTTAATAACATTAATTTTGGATCCTACATTTGCTGGAGATCCTATTTTA
 pv16coxI TCAGATTTACATTTTAATAACATTAATTTTGGATCCTACATTTGCTGGAGATCCTATTTTA
 pv32coxI TCAGATTTACATTTTAATAACATTAATTTTGGATCCTACATTTGCTGGAGATCCTATTTTA
 pv37coxI TCAGATTTACATTTTAATAACATTAATTTTGGATCCTACATTTGCTGGAGATCCTATTTTA
 po35coxI TCAGATTTACATTTTAATAACATTAATTTTGGATCCTACATTTGCTGGAGATCCTATTTTA
 pm58coxI TCAGATTTACATTTTAATAACATTAATTTTGGATCCTACATTTGCTGGAGATCCTATTTTA

781 840
 pfcoxI TATCAACATTTATTCCTGGTTTGTGGACATCCTGAAGTATACATTTTAATATTACCTGCT
 pf47coxI TATCAACATTTATTCCTGGTTTGTGGACATCCTGAAGTATACATTTTAATATTACCTGCT
 pv15coxI TATCAACATCTATTTTGGTTTGTGGACATCCTGAAGTGTATATTTTAATATTACCAGCA
 pv16coxI TATCAACATCTATTTTGGTTTGTGGACATCCTGAAGTGTATATTTTAATATTACCAGCA
 pv32coxI TATCAACATCTATTTTGGTTTGTGGACATCCTGAAGTGTATATTTTAATATTACCAGCA
 pv37coxI TATCAACATCTATTTTGGTTTGTGGACATCCTGAAGTGTATATTTTAATATTACCAGCA
 po35coxI TATCAACATCTATTTTGGTTTGTGGACATCCTGAAGTGTATATTTTAATATTACCAGCA
 pm58coxI TATCAACATCTATTTTGGTTTGTGGACATCCTGAAGTGTATATTTTAATATTACCAGCA

FIG. 10G

		841	900
PfcoxI		TTTGGAGTAATTAGTCATGTAATTTCTACTAATTAATGCAGAAATCTATTTGGTAATCAA	
Pf47coxI		TTTGGAGTAATTAGTCATGTAATTTCTACTAATTAATGCAGAAATCTATTTGGTAATCAA	
Pv15coxI		TTTGGTGTTATTTAGTCATGTAATATCTACAAATTAATTTGTAGAAGTTTATTTGGTAATCAA	
Pv16coxI		TTTGGTGTTATTTAGTCATGTAATATCTACAAATTAATTTGTAGAAGTTTATTTGGTAATCAA	
Pv32coxI		TTTGGTGTTATTTAGTCATGTAATATCTACAAATTAATTTGTAGAAGTTTATTTGGTAATCAA	
Pv37coxI		TTTGGTGTTATTTAGTCATGTAATATCTACAAATTAATTTGTAGAAGTTTATTTGGTAATCAA	
Po35coxI		TTTGGTGTTATTTAGTCATGTAATATCTACAAATTAATTTGTAGAAGTTTATTTGGTAATCAA	
Pm58coxI		TTTGGTGTTATTTAGTCATGTAATATCTACAAATTAATTTGTAGAAGTTTATTTGGTAATCAA	
		901	960
PfcoxI		TCATATGATACCTTGCTATGGGATGTATAGCTGTTTTAGGAAGCTTAGTATGGGTACATCAT	
Pf47coxI		TCATATGATACCTTGCTATGGGATGTATAGCTGTTTTAGGAAGCTTAGTATGGGTACATCAT	
Pv15coxI		TCATATGATTTTAGCAATGAGTTGTATTGCTATATATTAGGAAGTGTGTATGGGCTCATCAT	
Pv16coxI		TCATATGATTTTAGCAATGAGTTGTATTGCTATATATTAGGAAGTGTGTATGGGCTCATCAT	
Pv32coxI		TCATATGATTTTAGCAATGAGTTGTATTGCTATATATTAGGAAGTGTGTATGGGCTCATCAT	
Pv37coxI		TCATATGATTTTAGCAATGAGTTGTATTGCTATATATTAGGAAGTGTGTATGGGCTCATCAT	
Po35coxI		TCATATGATTTTAGCAATGAGTTGTATTGCTATATATTAGGAAGTGTGTATGGGCTCATCAT	
Pm58coxI		TCATATGATTTTAGCAATGAGTTGTATTGCTATATATTAGGAAGTGTGTATGGGCTCATCAT	

FIG. 10H

	961	1020
PfcoxI	ATGTACACTACTGGTTTAGAAGTTGATAC	TAGAGCTTATTTTACTTCGACTACCATTTTA
Pf47coxI	ATGTACACTACTGGTTTAGAAGTTGATAC	TAGAGCTTATTTTACTTCGACTACCATTTTA
Pv15coxI	ATGTATACTACAGGTTTAGAAGTAGATA	CAAGAGCATTTTTTACATCTACAACATATATA
Pv16coxI	ATGTATACTACAGGTTTAGAAGTAGATA	CAAGAGCATTTTTTACATCTACAACATATATA
Pv32coxI	ATGTATACTACAGGTTTAGAAGTAGATA	CAAGAGCATTTTTTACATCTACAACATATATA
Pv37coxI	ATGTATACTACAGGTTTAGAAGTAGATA	CAAGAGCATTTTTTACATCTACAACATATATA
Po35coxI	ATGTATACTACAGGTTTAGAAGTAGATA	CAAGAGCATTTTTTACATCTACAACATATATA
Pm58coxI	ATGTATACTACAGGTTTAGAAGTAGATA	CAAGAGCATTTTTTACATCTACAACATATATA

	1021	1080
PfcoxI	ATATCAATACCTACCGGTACAAAAGTAT	TAACTGGATATGTACATATATGAGTAGTAAT
Pf47coxI	ATATCAATACCTACCGGTACAAAAGTAT	TAACTGGATATGTACATATATGAGTAGTAAT
Pv15coxI	ATATCTATACCTACTGGAAACAAAATA	TATTTAAATGGATATGTACATATATGGGTAGTAAT
Pv16coxI	ATATCTATACCTACTGGAAACAAAATA	TATTTAAATGGATATGTACATATATGGGTAGTAAT
Pv32coxI	ATATCTATACCTACTGGAAACAAAATA	TATTTAAATGGATATGTACATATATGGGTAGTAAT
Pv37coxI	ATATCTATACCTACTGGAAACAAAATA	TATTTAAATGGATATGTACATATATGGGTAGTAAT
Po35coxI	ATATCTATACCTACTGGAAACAAAATA	TATTTAAATGGATATGTACATATATGGGTAGTAAT
Pm58coxI	ATATCTATACCTACTGGAAACAAAATA	TATTTAAATGGATATGTACATATATGGGTAGTAAT

FIG. 10I

	1081	1140
PfcoxI	TTTGGGTATGATACACAGCTCTTCATTATTGTTCATTATTATTTATATGTACATTTTACATTT	
Pf47coxI	TTTGGGTATGATACACAGCTCTTCATTATTGTTCATTATTATTTATATGTACATTTTACATTT	
Pv15coxI	TTTGGGTATAACTCATAGTTTCATCTTTATTATTCATTACTATTATATGTACATTTTACTTTT	
Pv16coxI	TTTGGGTATAACTCATAGTTTCATCTTTATTATTATCATTACTATTATATGTACATTTTACTTTT	
Pv32coxI	TTTGGGTATAACTCATAGTTTCATCTTTATTATTATCATTACTATTATATGTACATTTTACTTTT	
Pv37coxI	TTTGGGTATAACTCATAGTTTCATCTTTATTATTATCATTACTATTATATGTACATTTTACTTTT	
Po35coxI	TTTGGGTATAACTCATAGTTTCATCTTTATTATTATCATTACTATTATATGTACATTTTACTTTT	
Pm58coxI	TTTGGGTATAACTCATAGTTTCATCTTTATTATTATCATTACTATTATATGTACATTTTACTTTT	

	1141	1200
PfcoxI	GGAGGTACTACTGGAGTTATATTAGGTAATGCTGCCATTGATGTAGCATTACATTACATGACACA	
Pf47coxI	GGAGGTACTACTGGAGTTATATTAGGTAATGCTGCCATTGATGTAGCATTACATGACACA	
Pv15coxI	GGTGGTACTACAGGAGTAAATATTAGGTAATGCGAGCTATTGATATTGCATTACATGATACT	
Pv16coxI	GGTGGTACTACAGGAGTAAATATTAGGTAATGCGAGCTATTGATATTGCATTACATGATACT	
Pv32coxI	GGTGGTACTACAGGAGTAAATATTAGGTAATGCGAGCTATTGATATTGCATTACATGATACT	
Pv37coxI	GGTGGTACTACAGGAGTAAATATTAGGTAATGCGAGCTATTGATATTGCATTACATGATACT	
Po35coxI	GGTGGTACTACAGGAGTAAATATTAGGTAATGCGAGCTATTGATATTGCATTACATGATACT	
Pm58coxI	GGTGGTACTACAGGAGTAAATATTAGGTAATGCGAGCTATTGATATTGCATTACATGATACT	

FIG. 10J

	1201		1260
pfcoxI	TATTATGTTATTGCTCATTTCCATTTTGTA	CTATCAA	TTGGTGCAATTATTGGATTATTT
pf47coxI	TATTATGTTATTGCTCATTTCCATTTTGTA	CTATCAA	TTGGTGCAATTATTGGATTATTT
pv15coxI	TACTATGTAATCGCTCATTTCCATTTTGTA	TATCTA	TAGGTGCAATTATTGCAATTGTTT
pv16coxI	TACTATGTAATCGCTCATTTCCATTTTGTA	TATCTA	TAGGTGCAATTATTGCAATTGTTT
pv32coxI	TACTATGTAATCGCTCATTTCCATTTTGTA	TATCTA	TAGGTGCAATTATTGCAATTGTTT
pv37coxI	TACTATGTAATCGCTCATTTCCATTTTGTA	TATCTA	TAGGTGCAATTATTGCAATTGTTT
po35coxI	TACTATGTAATCGCTCATTTCCATTTTGTA	TATCTA	TAGGTGCAATTATTGCAATTGTTT
pm58coxI	TACTATGTAATCGCTCATTTCCATTTTGTA	TATCTA	TAGGTGCAATTATTGCAATTGTTT

	1261		1320
pfcoxI	ACAACTGTAAGTGCATTTCAAGATAA	TTCTTT	TGGTAAAAA
pf47coxI	ACAACTGTAAGTGCATTTCAAGATAA	TTCTTT	TGGTAAAAA
pv15coxI	ACATTAGTAAGTAGTTTTC	AAAGAAA	ACTTTTACCGTGAAAAATTC
pv16coxI	ACATTAGTAAGTAGTTTTC	AAAGAAA	ACTTTTACCGTGAAAAATTC
pv32coxI	ACATTAGTAAGTAGTTTTC	AAAGAAA	ACTTTTACCGTGAAAAATTC
pv37coxI	ACATTAGTAAGTAGTTTTC	AAAGAAA	ACTTTTACCGTGAAAAATTC
po35coxI	ACATTAGTAAGTAGTTTTC	AAAGAAA	ACTTTTACCGTGAAAAATTC
pm58coxI	ACATTAGTAAGTAGTTTTC	AAAGAAA	ACTTTTACCGTGAAAAATTC

FIG. 10K

	1321	1380
p _f coxI	GTAA TACTATGGTCAATGTTATTTTGTAGGTGTAATATTAAACATTTTACCTATGCAT	
p _f 47coxI	GTAATACTATGGTCAATGTTATTTTGTAGGTGTAATATTAAACATTTTACCTATGCAT	
p _v 15coxI	ATAATATTATGGTCAATCTTATTTTATTGGAGTTGTATTAAACATTTCTTACCTATGCAT	
p _v 16coxI	ATAATATTATGGTCAATCTTATTTTATTGGAGTTGTATTAAACATTTCTTACCTATGCAT	
p _v 32coxI	ATAATATTATGGTCAATCTTATTTTATTGGAGTTGTATTAAACATTTCTTACCTATGCAT	
p _v 37coxI	ATAATATTATGGTCAATCTTATTTTATTGGAGTTGTATTAAACATTTCTTACCTATGCAT	
p _o 35coxI	ATAATATTATGGTCAATCTTATTTTATTGGAGTTGTATTAAACATTTCTTACCTATGCAT	
p _m 58coxI	ATAATATTATGGTCAATCTTATTTTATTGGAGTTGTATTAAACATTTCTTACCTATGCAT	

	1381	1440
pfcx1	TTTATTAGGATTTAATGTAATGCCCTAGACGTAATTCCTGATTATCCAGACGCTTTAAATGGA	
pf47cox1	TTTTTAGGATTTAATGTAATGCCCTAGACGTAATTCCTGATTATCCAGACGCTTTAAATGGA	
pv15cox1	TTTCTTTGGATTTAAATGTAATGCCCTAGACGTAATTCCTGATTATCCAGACGCTTTAAATGGA	
pv16cox1	TTTCTTTGGATTTAAATGTAATGCCCTAGACGTAATTCCTGATTATCCAGACGCTTTAAATGGA	
pv32cox1	TTTCTTTGGATTTAATGTAATGCCCTAGACGTAATTCCTGATTATCCAGACGCTTTAAATGGA	
pv37cox1	TTTCTTTGGATTTAATGTAATGCCCTAGACGTAATTCCTGATTATCCAGACGCTTTAAATGGA	
po35cox1	TTCCCTTTGGATTTAAATGTAATGCCCTAGACGTAATTCCTGATTATCCAGACGCTTTAAATGGA	
pm58cox1	TTCCCTTTGGATTTAATGTAATGCCCTAGACGTAATTCCTGAT.....	

FIG. 10L

	1441		1500
PfcoxI		TGGAATATGATTTGTTCTATGGGTCAACAATGACTTTATTGGTTACTTAATTTTAAA	
Pf47coxI		TGGAATATGATTTGTTCTATGGGTCAACAATGACTTTATTGGTTACTAATTTTAAA	
Pv15coxI		TGGAATATGATTTGTTCAATGGATCAACAATGACTTTATTGGTTATATTAAA	
Pv16coxI		TGGAATATGATTTGTTCAATGGATCAACAATGACTTTATTGGTTATTTAAA	
Pv32coxI		TGGAATATGATTTGTTCAATGGATCAACAATGACTTTATTGGTTATTTAAA	
Pv37coxI		TGGAATATGATTTGTTCAATGGATCAACAATGACTTTATTGGTTATTTAAA	
Po35coxI		TGGAATATGATTTGTTCAATGGATCAACAATGACTTTATTGGTTATTTAAA	
Pm58coxI		

	1501		1560
PfcoxI		TAATATTAC.TATTTATTGTTTTATGAACCTTTACTCTATTAAATTTAGTTAAAGCACAC	
Pf47coxI		TAATATTAC.TATTTATTGTTTTATGAACCTTTACTCTATTAAATTTAGTTAAAGCACAC	
Pv15coxI		TAATATAAAAATATTTTGTTTATATGAATTATTATTCTATTAAATTTAGCAAAAGCACAT	
Pv16coxI		TAATATAAAAATATTTTGTTTATATGAATTATTATTCTATTAAATTTAGCAAAAGCACAT	
Pv32coxI		TAATATAAAAATATTTTGTTTATATGAATTATTATTCTATTAAATTTAGCAAAAGCACAT	
Pv37coxI		TAATATAAAAATATTTTGTTTATATGAATTATTATTCTATTAAATTTAGCAAAAGCACAT	
Po35coxI		TAATATAAAAATATTTTGTTTATATGAATTATTATTCTATTAAATTTAGCAAAAGCACAT	
Pm58coxI		

FIG. 10M

43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

	1561		1584
PfcoxI	TTAATAAAATTACCCCATGTCCATTG		
Pf47coxI	TTAATAAAATTACCCCATGTCCATTG		
Pv15coxI	TTATTAAATTTACCCCATGTCCATTG		
Pv16coxI	TTATTAAATTTACCCCATGTCCATTG		
Pv32coxI	TTATTAAATTTACCCCATGTCCATTG		
Pv37coxI	TTATTAAATTTACCCCATGTCCATTG		
Po35coxI	TTATTAAATTTACCCCATGTCCATTG		
Pm58coxI		

FIG. 10N

559080-2559260

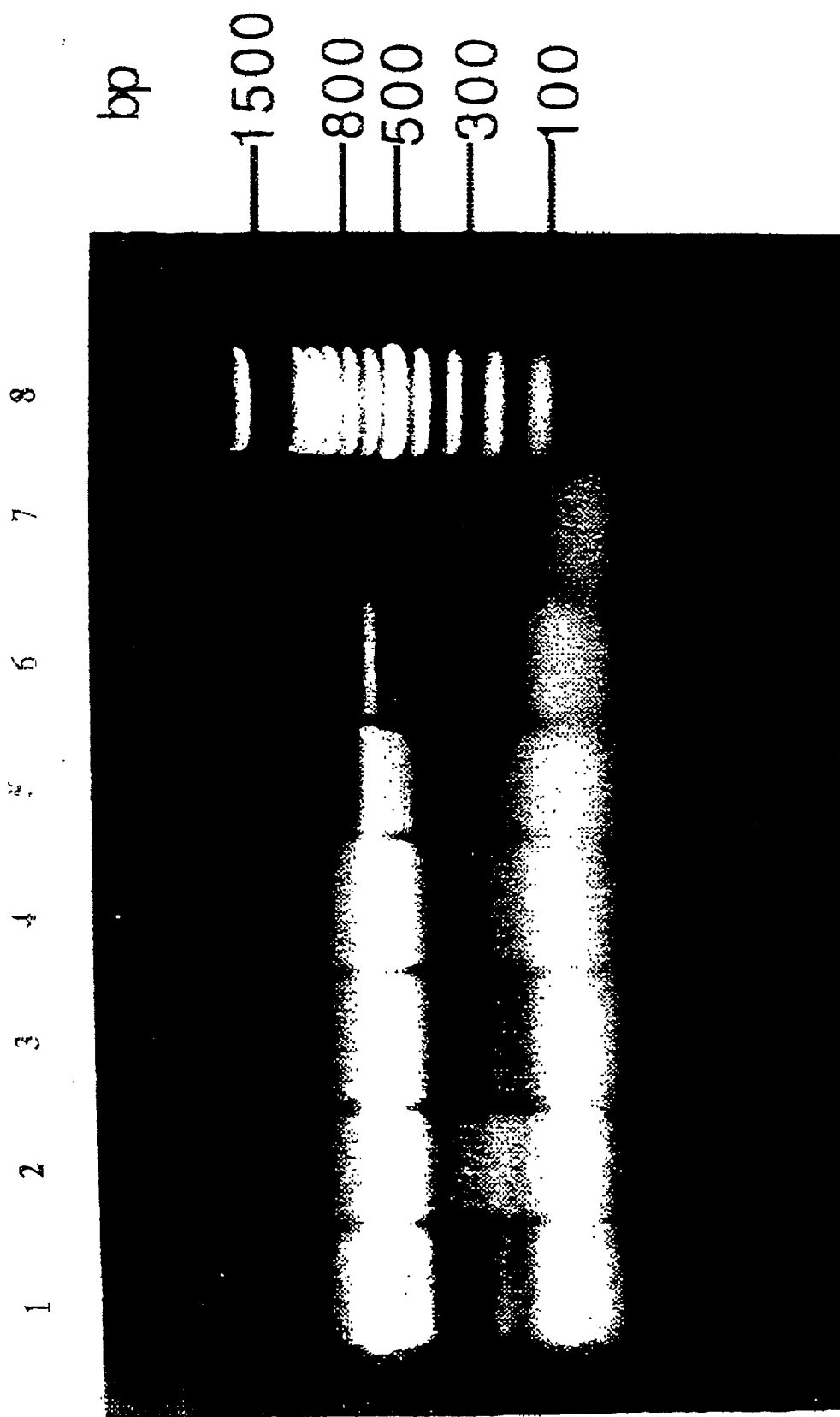


FIG. 11